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Hamud, Fozia

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Fozia Hamud **Patent Examiner** Art Unit 1647 Crystal-Mall-One, Room 10Bo5 Mail Box CM1-10B19 308-8891

Point of Contact: **Toby Port** Technical Info. Specialist CW1 6A04 703-308-3534

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	onu - ote	Run on: May 12, 2003, 10:35:27; Search time 357 Seconds (Without alignments) 15032.246 Million cell		able: IDENTITY_NUC Gapop 10.0 ; Gapext 1:0	Searched: 2185239 seqs, 1125999159 residues Total number of hits satisfying chosen parameters		Post-processing: Minimum Match 0% Maximum Match 100% Tathor first As summarise	Database : N.Geneseq_101002:*	त्त्त्	* ; /SLDSZ/gogdatz/geneseg/genesegn-embL/NA1983.DAT 5: /SIDSZ/gogdatz/geneseg/genesegn-embL/NA1984.DAT 6: /SIDSZ/gogdatz/geneseg/genesegn-embL/NA1985.DAT	/SIDS1/gcgdata/geneseq/geneseqn-embl/NP /SIDS1/gcgdata/geneseq/geneseqn-embl/NP /SIDS1/gcgdata/geneseq/geneseqn-embl/NP	10: /SIDSZ/gcgdata/geneseg/genesegn-embl/NA1989.DAT 11: /SIDSZ/gcgdata/geneseg-embl/NA1990.DAT 12: /SIDSZ/gcgdata/geneseg-embl/NA1990.DAT	genesedn embl/ genesedn-embl/ genesedn-embl/	13: /SlbS/yGgdata/geneseg/yenesegn-emb//NA1994,1AT 16: /SIDS/yGgdata/yeneseg/yenesegn-emb//NA1995,DAT 17: /SIDS/yGgdata/xeneseg/yenesegn-emb//NA1995,DAT	// SIDS2/gcgdata/geneseq/genesequembl/	/SIDS2/gcgdata/genesed/genesedn-embl/k	/SIDS//gcgdata/geneseq/geneseqn.embl/ /SIDS//gcgdata/geneseq/geneseqn-embl/ /SIDS//gcgdata/geneseq/geneseqn-embl/ /SIDS//gcgdata/naneseq/geneseqn-embl/			SUMMARIES	Query Score Match Length DB ID Descr	100.0 2383 24, ABA95031	99.7 2381 96.1 2341 93.1 2786	2215.4 93.0 3083 23 AAS15346 2158.4 90.6 4392 24 ABK62082	87.0 2319 22 AAS09517

Murine interleukin Murine interleukin Murine Interleukin Murine IL-17R poly Human cancer cell

Human adenosine Al Micromonospora DNA Human immune/haema Human cervical can Human cDNA encodin

Gao Z;

Presnell SR, Kuestner RE, (ZYMO ) ZYMOGENETICS INC.

P-PSDB; ABB07626.

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New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ligand.

Claim 5; Page 85-90; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Scytoria Fine Scytoria polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis of two or growth. The encoding nucleic acids are useful for providing Scytoria in vivo by gene therapy techniques. Ecytoria oligonucleotide probes are useful for in vivo diagnosis, and the Scytoria probes and primers can be used to detect and localize Scytoria gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which scytoria gene resides. The Scytoria polymucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familia. Euclodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Ecytoria nucleotide sequence. 

Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 other;

240 300 360 420 180 240 CAAATATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGC 360 480 GAAGTCGGAGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAG 540 GGCCTGGCTGGGCGAGCGCACGGCCATGGCCCCGTGGCTGCAGCTCTGCTCCTTCTT 120 Gaps TGTTGCTAATGAGGAGTGGGGCCAGCAGCAGAAACAGTGGGCTGTACAACACTT TGTTGCTAATGAGGGAGTGGGGCCAGCCAGCAGAAACAGTGGGCTGTACAACATCACCTT CCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTG TACGGTCAACGCCTGCCTCAACGCCTCGCAGCTGTGGCCGCTGGCCGGGTCCGGCCG CGCGCGGGGGCGCCGACACCTGTGGCTGGAGGGAGAAAGCGGCTGCCCGGACCCCGGCTTTG GTCCCCAGGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCT TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGA TTATTTCGTAAAGGTTGTCCCTTTTCCTTCCATTAAAAACGAAAGCAATTACCACCCTTT Ouery Match 100.0%; Score 2383; DB 24; Length 2383; Best Local Similarity 100.0%; Pred. No. 0; Matches 2383; Conservative 0; Mismatches 0; Indels 0; 61 61 121 181 181 241 361 481 601 121 241 301 301 361 421 481 421 ð đ ò g ò 윱 ö 셤 à გ ò 셤 셤 ò g ò 셤 ò . 명 à õ

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New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand

Disclosure; Page 94-98; 119pp; English.

26-JUL-2000; 2000US-220747P

Presnell SR, Kuestner RE, (ZYMO ) ZYMOGENETICS INC.

WPI; 2002-217048/27. P-PSDB; ABB07627.

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1741 AGGCCGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGCCCGA 1800
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1681 CCAGGAGCCGGGGCACCACACGCGACAGGAACGAACTACTTCCGGAGCAAGTC
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The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psortasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for the vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are linkage-based testing of pulmonary alveolar proteinosis, familial linkage-based testing of pulmonary alveolar proteinosis, familial polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 variant nucleotide sequence.
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//tag= a /product= "Zcytor18 splice variant"
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receptor, Zcytor18 splice variant nucleotide sequence.

tor; Zcytor18; cell proliferation; antipsoriatic; human; colar proteinosis; familial periodic fever; antitumour; a; chromosome 3p14.3; gene therapy; splice variant; ds.

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                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated cytokine receptor polypeptide designated Ecytori8. The Ecytori8 polypeptides can be used to inhibit cell proliferation associated with polypeptides can be used to inhibit cell proliferation associated with polypeptides can be used to inhibit encombinant methodology. The polypeptides can be used to inhibit encoding nucleic acids are useful for providing Ecytori8 in vivo by gene therapy techniques Ecytori8 oligonucleotide probes are useful for in vivo diagnosis, and the Ecytori8 probes and primers can be used to detect and localize Ecytori8 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in Ecytories and in which Ecytorie gene resides. The Ecytorie polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial linkage-based testing of pulmonary alveolar proteinosis, familial polymorphisms of cytokine receptors. The present sequence represents a human Ecytorie spilor ever and erythic ever and erythic ever mucleotide sequence.
                                                                                                                                                                                                                                                   New cytokine receptor polypeptide designated zcytori8, useful for an inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ligand
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Query Match

Best Local Similarity 98.2%; Pred. No. 0;

Matches 2341; Conservative 0; Mismatches : 0; Indels 42; Gaps
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                                                                                                   26-JUL-2000; 2000US-220747P.
                                                                 23-JUL-2001; 2001WO-US23253.
                                                                                                                                                                              Kuestner RE,
                                                                                                                                        (ZYMO ) ZYMOGENETICS INC
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P-PSDB; ABB07628.
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CCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTG 420

1158 1218 1021 CAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCAC 1080 CTTTCTCTGCTATTCCAGTAAAGATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGC 1260 1320 CCTCTGTAGAGAAGGGCAGAGAGATGGGTCATCCAGAAGATCCACGAGTCCCAGTTCAT 1380 1399 AGGAGGTGGCCGAGGCTCGGGGAAAGGAAAGCTCTTCCTGGTGGGGGTGTCAGCCATTGC 1458 678 438 540 498 9 780 840 CGAAGGACCTTTCAAGCGAAAGACTGTAAGCAGGAGCAAACTACAGAGACACCACCAG 900 960 918 9 558 618 720 799 CGAAGGACCTTTCAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACCAGCTG 858 GTCCCCAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCT GAAGTCGGAGGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAG 541 TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGA TTATTTCGTAAAGGTTGTCCCTTTCCTTCCATTAAAAACGAAAGCAATTACCACCCTTT CTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACC CTICTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGCAGGTGTCCTT CGACCATGCACCGCACAACTTCGGCTTCCGTTTCTTCTTCTTCACTACAAGCA 901 CCTCCTTCAAAATGTTTCTCCAGGGATTATAAATTGAGCTGGTGGATGACACTAACAC TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGGCTCCGGCCGCGGCCGAAGGT 1441 AGGAGGTGGCCGAGGCTCGGGGAAAGGAGGCTCTTCCTGGTGGCGGTGTCAGCCATTGC 1501 合 a õ ö

Location/Qualifiers 70.1286

23-MAY-2001; 2001WO-US16767. 24-MAY-2000; 2000US-206862P. (SCHE ) SCHERING CORP.

WO200190358-A2. 29-NOV-2001.

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Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -

WPI; 2002-106198/14. P-PSDB; AAU11355

Gorman DM;

Claim 16; Page 21-25; 148pp; English.

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The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynculectides encoding them. The receptors, or their portions may be useful; as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antipodies capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen. A combination of antiser or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the human DCRSB polypeptide.
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Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; ss; gene therapy; protein therapy; immunological disorder.

Homo sapiens

Human DNAX cytokine receptor subunit 8 (DCRS8) cDNA.

26-MAR-2002 AAS18134;

AAS18134 standard; cDNA; 2786 BP

us-09-912-157-1.rng

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	a x	A encoding human interleukin 17 (hIL-17) receptor lik	•~
	<b>X</b>	KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;	

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anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;

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Location/Qualifiers

/product- "Interleukin 17 (IL-17) receptor like protein" /note= "No stop codon glven" 16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460. 15-MAR-2001; 2001WO-US08678 /partial /\*tag= (AMGE-) AMGEN INC. WO200168859-A2 20-SEP-2001

Jing S;

WPI; 2001-611392/70. P-PSDB; AAU09904

receptor like polypeptides, treating, e.g. leukaemia, asthma, Nucleic acids encoding interleukin 17 useful for preventing, diagnosing and diabetes, psoriasis and glaucoma -

Claim 1; Page 147-148,150-151; 158pp; English.

Sequence 3083 BP; 782 A; 807 C; 767 G; 727 T; 0 other;

Gaps DB 23; Length 3083; Indels 42; 9 Query Match 93.0%; Score 2215.4; Best Local Similarity 97.9%; Pred. No. 0; Matches 2271; Conservative 0; Mismatches

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1144 AGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGGCCCATCAGA 1024 1025 GCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTG 1084 664 558 618 678 978 120 ------GGGAGTGGGCCAGCCAGCAGAACAGTGGGCTGTACAACATCACCTTCAAA 198 199 TATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAG 258 424 TCGGAGGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGC 544 724 844 679 CACGCACCGCACAACTTCGGCTTCCGTTTCTTCTTCTTCACTACAAGCTCAAGCACGAA 738 184 244 305 TATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAG 364 TEGAAGCCTCEGAACCTGAACATCAGCCAGCATGGCTCGGACATGCAGGTGTCCTTCGAC 784 GGACCTTTCAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACCAGCTGCCTC 904 CTICAAAAIGITICICCAGGGGATIATAATIGAGCIGGIGGATGACACTAACACAACA 964 124 GCTAATGAGGGAGTGGGGCCAGCCAGCAGAACAGTGGGCTGTACAAAACATCACCTTCAAA 304 9 TGGCTGGCCGAGCCCACGGCCATGGCCCCGTGGCTGCAGCTCTGCTCCTTCTTACG 919 GCCATGGCCATCACAGTGCCACTGGTAGTCGGCATTCGCGACGCTCTTCACTGTG 125 GTCAACGCCTGCCTCAACGCCTCGCAGCTGGCTGTGGCCGCTGGCGGGTCCGGCCGCGGC 185 CGGGGCGCCGACACCTGTGGCTGGAGGATGAAAGCGGCTGCCCGGACCCCGGCTTTGTGTT AATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCC TTCGTAAAGGTTGTCCCTTTTCCTTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTC TITAGAACCCGAGCCTGTGACCTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTC CATGCACGCACAACTTCGCCTTCCTTCTATCTTCACTACAAGCTCAAGACGACGAA **ATGTGCCGCAAGAAGCAACAAGAAATATATATTCACATTTAGATGAAGAGACTCTGAG** 1 rescressorance are respected and respected and respect to the respect of the respect to the re 121 TGGGGCGTCGACACCTGTGGCTGGAG------605 725 845 905 965 1085 485 99 785 65 365 245 147 19 a 용 윱 셤 셤 a g 셤 g ð 셤 셤 à a õ q ð 셤 ò 셤 ð ð 셤 à à ð ð ò ŏ ð ç

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arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease, meningitis, encephalitis, neoplasia, trauma, lasheama and infarction, amania, stroke, cardiovascular disease, atheroscierosis, rheumatoid arthritis, hypothyroidism, anaemia, sepsis, allergic responses, multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides and polynucleotides of secreted proteins useful for treating various diseases such as multiple sclerosis, cancer, autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's
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                                CTCTGCTATTCCAGTAAAGATGGCCAGAATCACATGAATGTCGTCGTCCAGTGTTTCGCCTAC
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Human; ss; gene; secreted protein; cancer; autoimmune disease; arthritis; osteoporosis; Alzheimer's disease; Parkinson's disease; meningitis; encephalitis; neoplasia; trauma; ischaemia; infarction; mania; stroke; cardiovascular disease; atheroscierosis; sepsis; anaemia; rheumatoid arthritis; hypothyroidism; allergic response; liver failure; multiple sclerosis; haemorrhage; paranola; obsessive compulsive disorder; autism; panic disorder; learning disability; feeding disorder; sleep pattern disorder; balance; perception; Thi-dependent insulitis; adult respiratory distress syndrome; ARDS.
                                                                               2119 TCAGGCCTGGGTGAGGAGGAACCTCCTGCCTTCCTTCCAAGCTCCTCTTCTGGGTCA 2178
                                          TGCAAAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCTTTG
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ņ sclerosis, liver failure, haemorrhages, paranola, obsessive compulsive disorder, autism, panto disorder, learning dissbillities, ALS (amylotrophic lateral sclerosis) psychoses, disorders in feeding sleep patterns, balance, and perception, Thi-dependent insulitis, adult respiratory distress syndrome (ARDS). The secreted protein is further useful for identifying compounds that bind to the secreted protein The present sequence encodes a novel secreted protein of the invention. 145 . 589 265 385 258 GCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATCGAA 445 505 565 438 625 558 745 618 802 678 925 798 Gaps 9 TTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCACCCATCAGCCAGTAT CCTTCCATTAAAAACGAAATTACCACCCTTTCTTTTAGAACCCGAGCCTGTGAC TGTAAGCAGGAGCAAACTACAGAGACGACCAGCTGCCTCCTTCAAAATGTTTCTCCAGGG TGGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTGCTAATGAGGGAGTGGGGGCCA TTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGGGAAGACAGTGCCAA TCTCAACCTTTCCTGAATATGAAACTTGAAACGGATTATTTCGTAAAGGTTGTCCCTTTT DB 24; Length 4392; 46; BP; 1125 A; 1050 C; 1101 G; 1116 T; 0 other; 90.64; Score 2158.4; DB 24; Lengt llarity 98.04; Pred. No. 0; Conservative 0; Mismatches 1; Indels ١, Local Similarity les 2255; Conserv Sequence 4392 Match Best Loc 86 146 19 902 121 998 139 326 199 386 259 446 319 206 379 999 139 979 661 989 559 746 619 908 629 998 739 326 Query 88888888 ð 윱 8 윱 ò 윱 g à 8 8 ð g ö ò 셤 ç 셤 ö 셤 ŏ 셤 à ò 쉽 å 셤 õ ద ç ç

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                    2062 CCTGCTGCACACGGTGAAAGCCGGCAGCCCTCGGACATGCCGCGGGACTCAGGCATCTA, 2121
                                                                2122 TGACTCGTCTGTGCCCTCATCCGAGCTGTCTGCCACTGATGGAAGGACTCTCGACGGA 2181
                                                                                                            2182 CCAGACAGAAACGTCTTCCCTGACGGAGAGAGTGTCCTCCTCTTCAGGCCTGGGTGAGGA 2241
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; ss; PRO20026; DNA 154095-2998; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; astima; demyelinating disease; degenerative cartilaginous disorder; transplantation associated diseasether.
                                                                                                                          Buman cDNA encoding Interleukin 17 receptor, IL-17RH4..
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/product= "IL-17RH4"
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10-NOV-2000;
28-NOV-2000;
01-DEC-2000;
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18-FEB-2000;
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The sequence (DNA 154095-2998) encodes a PRO polypeptide (PRO20026)
which is the human Interleukin 17 receptor, IL-17RH4. A composition
containing ant/agonists to the PRO polypeptides or individual components
containing ant/agonists to the PRO polypeptides or individual components
containing ant/agonists to the PRO preptides or individual components
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
livenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
idopathic-inflammatory myopathy. Sjogren's syndrome, systemic
containing arthritis; and emolytic; aneania, autoimmune
clisease, a demyelinating disease, an autoimmune or immune-mediated renal
disease, contact demantitis; an allergic disease or food
hypersensitivity asthma, a transplantation associated disease, or a
chronic inflammatory demyelinating polyneuropathy. Treating a PRO1031 or
degenerative cartilaginous disorder comprises administering a PRO1031 or
PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
examples of the diseases and disorders are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGG 431
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                         Vandlen
                                                                                                                                                                                                                     Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes -
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                         ', Tumas D, Van Look
Wood WI, Yansura DG;
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Gurney AL, L1 H, Hillan K
Watanabe CK, Williams PM,
                                                                                                                   WPI; 2001-451708/48.
P-PSDB; AAU04958.
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                                               933 TAATTGAGCTGGTGGATGACACTAACACAAGAAAAGTGATGCATTATGCCTTAAAGC 992
                                                                                                     TAATTGAGCTGGTGGATGACACTAACACAAGAAAAGTGATGCATTATGCCTTAAAGC 901
CGCATGGCTCGGACATGCAGGTGTCCTTCGACCACGCACCGCACAACTTCGGCTTCCGTT 721
                                                                                                                                                                                                                                                               TCCAGAAGATCCACGAGTCCCAGTTCATCATTGTGGTTTGTTCCAAAGGTATGAAGTACT
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1893 ATGATGTCATGTGCAAACCAGGGCCTGAGAGTGACTTCTGCCTAAAGGTAGAGGCGGCTG
                     1802 ATGATGTCATGTGCAAACCAGGGCCTGAGAGTGACTTCTGCCTAAAGGTAGAGGCGGCTG
                                                                                    1953 TTCTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGAGTCAGCATGGGGGCCTGGACC
                                                                                                                             1862 TTCTTGGGGCAACCGGACCAGCGACTCCCAGCACGAGAGTCAGCATGGGGGCCTGGACC
                                                                                                                                                                      AAGACGGGGAGGCCCGGCCTGCCCTTGACGGTAGCGCCGCCCTGCTACCCCTGCTGCTGCACA
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/*tag= a
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New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand

Claim 7; Page 111-115; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Ecytor18. The Ecytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psorlasis or tumour growth. The encoding nucleic acids are useful for providing Ecytor18 in vivo by gene therapy techniques. Ecytor18 oligonocleotide probes are useful for invivo diagnosis, and the Ecytor18 probes and Minners can be used to detect and localize Ecytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chicmosome 3 in which Ecytor18 gene resides. The Ecytor18 polypucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial polymorphisms of cytokine receptors. The present sequence represents a murine Ecytor18 nucleotide sequence.

Sequence 2443 BP; 564 A; 700 C; 642 G; 537 T; 0 other;

Query Match 68.8%; Score 1638.4; DB 24; Length 2443; Best Local Similarity 82.5%; Pred. No. 0; Matches 1976; Conservative 0; Mismatches 356; Indels 64; C Query Match

GAACGGCCTGGCTGGGCGAAGGCCATGGCCCCGTGGTGCAGCTCTGCTCCGTCT 116 GCCGCGCGCGCGCCGACACCTGTGGCTGGAGGATGAAAGCGGCTGCCCGACCCCGGC 236 TITGIGITGCTAATGAGGGAGTGGGGCCAGCCAGCAGAACACTGGGCTGTACAACATCA 296 CCGCCGCGCCACCCCCACTCGGGGCT----GGCCAGCGGCGGGCGGCCGGGGCGCAGA 56 12 117 132 177 237 22 . G ö 윱 à 뭐 8 q ŏ a

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CCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGT---GGGGAAGCATGTGATTG 353 TTCTTTGGTCCCCAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGG 473 TCAACAGTAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTG 593 390 TICTTTGGTCCCCAGGGGCCCTTGGCATTGAATTCCTAAAAGGATTCCGAGTCATCCTGG CTGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCA AGGAGCTGAAGTCGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGC 297 354 330 14 474 20 534 594 ò a 음 ð 셤 윱 ò ð ð 셤 à

AGG-----AGGTGCTGGGTCAGCACCCAGGCCACAGAAGAAGGAACTACTTCCGGA 1703 1734 GCAAGTCAGGCCGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGG 1793

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1014 GGCCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGC 1073 CTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGGCAGTGCACTCCCCGTGGGCCG 1013 ACTICAGCCTCTGTAGAGAGAGGGAGAGAATGGCTCATCCAGAAGATCCACGAGTCCC 1373 1434 AACACAAAGGAGGTGGCCGAGGCTCGGGGAAAGGAGAGCTCTTCCTGGTGGCGGTGTCAG 1493 1410 GACACAAAAGAGGCGCGCGCGGGGGGCGAAGGCGAGTCTTCCTGGTGCCGTGGCGC 1469 CCATTGCCGAAAAGCTCCGCCAGGCCAAGCAGATTCGTCCGCGGCGCTCAGCAAGTTTA 1553 1590 CCAAGTACAAGCTCATGGACCACCTCCTGAGCTCTGTGCCCATCTGCACAGGAGAGC 1649 AGTICATCATIGIGGITŢGTICCAAAGGIAIGAAGIACITIGIGGACAAGAAGAACIACA 1433 1554 TCGCCGTCTACTTTGATTATTCCTGCGAGGAGGACGTCCCCGGTATCCTAGACCTGAGTA 1613 TCAAGCACGAAGGACCTITCAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGAGG 893 930 GCAACACCACCAGGAAGCTGCTCATGTGGTGAAGTCAGTGCAGTGTCCCTGGGCTG 989 654 ACCCTTTCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGCCGGACAATCTAGCTT 713 TGTCCTTCGACCATGCACCGCACAACTTCGGCTTCCGTTTCTTCTTCTTCACTACAAGC 833 ATCCCTTCTTCTTCAGAACACGGGCCTGTGACTGTTGTTACAACCTGACAACTTGGCCT CCAAGTACAGACTCATGGACAATCTTCCTCAGCTCTGTTCCCACTTGCACTCCCGAGACC ACGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGCAGCAGGAAGGAACTACTTCCGGA 1254 1314 1374 1470 1674 630 069 774 750 834 810 066 1074 1494 1614 ð a Š 윱 ö 셤 ö 셤 ò g g a ð 윱 à g q g 윱 å ò g å 윱 ò 윱 ç q ò g õ ð

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                    AGCCCGACTGGTTCGAAAAGCAGTTCGTTCCTTCCATCCTCCTCCACTGCGCTACCGGG .1853
                               1854, AGCCAGTCTTGGAGAATTTGATTCGGGCTTGGTTTTAAATGATGTCATGTGCAAACCAG 1913
                                                                             GCCCTGAGAGTGACTTCTGCCTAAAGGTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAG 1973
                                                                                                                      1974 CCGAC-----TCCCCAGCACGAGGTCAGCGGGGCCTGGACCAAGACGGGGAGGCCC 2027
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Human cytokine receptor, Zcytor18 degenerate coding sequence. ABA95032 standard; DNA; 2259 BP. 20-MAY-2002 (first entry) ABA95032; RESULT 9 

Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; ds.

23-JUL-2001; 2001WO-US23253. 26-JUL-2000; 2000US-220747P (ZYMO ) ZYMOGENETICS INC. WO200208259-A2. Homo sapiens. 31-JAN-2002

Presnell SR,

P-PSDB; ABB07626.

New cytokine/receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation:associated with psoriasis or tumor growth; and modulating immune system by binding to endogenous zcytor18

Disclosure; Page 92-93; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Scytor18. The Zeytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell'proliferation associated with psortasis or tumour growth. The encoding nucleic acids are useful for providing Zeytor18 in vivo by gene therapy techniques. Ecytor18 oldponucleotide.probes are useful for in vivo diagnosis, and the Zeytor18 probes and primers can be used to detect and localize Zeytor18 gene expression in tissue samples. The probes are also useful for in vivo diagnosis, and the Zeytor18 probes are becaused in which Ecytor18 gene resides. The Zeytor18 probles and charactering in Certor18. Deliminary alveolar proteinosis, familial linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zeytor18 degenerate coding sequence. 

Sequence 2259 BP; 379 A; 234 C; 373 G; 293 T; 980 other;

GCCAGCAGAAACAGTGGGCTGTACAACATCAACATATGACAATTGTACCACCTAC 325 TTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCAGCATCAGCCAGTAT 385 241 YINAAYCCNGTNGGNAARCAYGTNATHGCNGAYGCNCARAAYATHACNATHWSNCARTAY 300 TTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGGGAAGACAGTGCCAA 505 TGGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTGTGTAATGAGGGAGTGGGCCA 265 181 GCNWSNMGNAAYWSNGGNYTNTAYAAYATHACNTTYAARTAYGAYAAYTGYACNACNTAY 240 GCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATCGAA 445 86 AIGGCCCCGIGGCIGCAGCICIGCICCICTITIAGGGICAACGCCIGCCICAACGGC 145 1 ATGGCNCCNTGGTTNCARYTNTGYWSNGTNTTYTTYACNGTNAAYGCNTGYYTNAAYGGN 60 Query Match
67.7%; Score 1614.4; DB 24; Length 2259;
Best Local Similarity 56.6%; Pred.:No. 0;
Matches, 1279; Conservative, 577; Mismatches 402; Indels 0; 206 566 326 386 446 ð 원 ð 윱 ð ð à

506 CAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAA 565 421 CARYTHATHYTHAARGAYCCHAARCARYTHAAYWSHWSNTTYAARMGNACNGGNATGGAR 480 TCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAAAGGTTGTCCCTTTT 625 CCTTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTTTAGAACCCGAGCCTGTGAC 685 626 . අ à 음 ò 셤 à ŏ à

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                                TIYCAYCCNCCNCCNYTNMGNIAYMGNGARCCNGTNYINGARAARTIYGAYWSNGGNYIN 1800
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ABA95034 standard; DNA; 2259 BP. RESULT 10

20-MAY-2002 (first entry)

ABA95034;

Cytokine receptor; Ecytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene:therapy; ds. Human cytokine receptor, Zcytor18 variant degenerate coding sequence

Homo saplens.

40200208259-A2.

23-JUL-2001; 2001WO-US23253. 31-JAN-2002.

26-JUL-2000; 2000US-220747P.

Presnell SR, Kuestner RE, (ZYMO) ZYMOGENETICS INC.

Gao 2;

WPI; 2002-217048/27. P-PSDB; ABB07627.

New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand -

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Disclosure, Page 101-102; 119pp; English

The invention relates to an isolated cytokine receptor polypeptide designated Ecytoria. The Ecytoria polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with peolasis or tumour growth. The cell proliferation associated with peolasis or tumour growth. The concoding nucleic acids are useful, for providing Ecytoria in vivo by gene therapy, techniques. Ecytoria oligonuclectide probes are useful for in vivo diagnosis, and the Ecytoria probes and primers can be used to detect and localize Ecytoria gines expression. In tissue/samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which inkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The presents a human Ecytoria variant degenerate coding sequence represents a

Sequence 2259 BP; 379 A; 234 C; 374 G; 293 T; 979 other;

0; Gaps 67.6%; Score 1612; DB 24; Length 2259; 56.6%; Pred. No. 0; Best Local Similarity 56.6%; Pred. No. 0; Matches 1278; Conservative 576; Mismatches 404; Indels Query, Match

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1 AIGGCNCCNIGGYINCARYINTGYMSNGTNTTYTTYACNGTNAAYGCNTGYYTNAAYGGN 60 98 146 셤 ö

265 TGGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTGCTAATGAGGGAGTGGGGCCA .19 902

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                                                                 2065
                                                                                                                                                                       New cytokine receptor polypeptide designated zcytor18, useful for growthing cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand
                                     1861 GCNGCNGTNYTNGGNGCNACNGGNCCNGCNGAYWSNCARCAYGARWSNCARCAYGGNGGN 1920
                                                                                                                                                                                                                                ACAGAAACGICTICCCTGACGGAGAGCGTGTCCTCTTTCAGGCCTGGGTGAGGAGGAA 2245
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                                                                               GCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGAGTCAGCATGGGGGC
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therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome. In which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 splice variant degenerate coding sequence.
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                                                                                                                                         CTCCCAAGAGAGAGGCTCCGGCCGGAGGTCTTTCTTCTTCTATTCCAGTAAAGAT 1225
                                                                                                                                                                                    GGCCAGAATCACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGTGGC 1285
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859 XTNAARCCNGTNCAYWSNCCNIGGGCNGGNCCNATHMGNGCNGTNGCNATHACNGTNCCN 918
                                                                                             CAGGGCAGCAGAAGGAACTACTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCATT
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The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polyunclectides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other crytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents human DCRS reverse translation generic cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; ss; gene therapy; protein therapy; immunological disorder.
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                                                                                                                        1998
                                                                                                                                                                                                                ACAGAAACGTCTTCCCTGACGGAGAGCGTGTCCTCTTCAGGCCTGGGTGAGGAGAA 2245
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                                                                                              TCGTCTGTGCCTCATCCGAGCTGTCTCTGCCACTGATGGAAGGACTCTCGACGGACCAC
                                                                                                                                                                                                                                                                                                                                            2306 CGCAGCTACACTGATGAACTCCACGCGGTCGCCCCTTT..2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DCRS8 reverse translation generic cDNA.
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G; 287 T; 975 other;

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ch Sallarity 54.7%; Pred. No. 0; 215; Conservative 566; Mismatche 411; Trocccccccccccccccccccccccccccccccccccc	2214; 45; Gaps 2;	145 60	CACCATGGC 205 CACCATGGC 205 CACCATGGC 205 CACCATGGGC 205 CACCATGGGCC 205 CACCATGGGCC 205 CACCATGGGCC 205 CACCATGGGCC 205 CACCATGGCCC 205 CACCATGGGCCC 205 CACCATGGCCC 205 CACCATGGCCCC 205 CACCATGGCCCC 205 CACCATGGCCCC 205 CACCATGGCCCC 205 CACCATGGCCCCC 205 CACCATGGCCCC 205 CACCATGGCCCCC 205 CACCATGGCCCCCCCCCC 205 CACCATGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	0y  TGAGGGGGCCCA 265                    Db  -NNNGGNGTNGGNCCN 138	32	385 258	445 318	QY 	565 438	625 495	685 555	745	805 ·	865 735	925 795	985 855	1045 915	AAGCAACAA 1105
13 2 1 2 2 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2	62.8%; Score 1496; DB 24 Similarity 54.7%; Pred. No. 0; j; Conservative 566; Mismatches 411	FGGCCCCGGGCGCGCGCTCCGCTCTTTTACGGTCACGCCTGC 	GGCAGCTGGCTGGCCGCTGGCGGGTCCGGCCGCGCGCGGGGGCGCCGAC :     :	GGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTGTAATGAGGGA	CCAGCAGAAACAGTGGGCTGTACAACATCACTTCAAATATGACAATTGT 	igaatccagtaggaagcatgtgattgctgacgcccagaatatcaccatc 	THECCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTC	CCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGGGAAGA 	aactgattctaaaggatccgaagcagctcaacagtagcttcaaaagaact   : :       : :       :	CICAACCTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAAAGGTT :   :	TTCCATTAAAAACGAAAGCAATTACCAGCCTTTCTTCTTTAGAACCCGA 	GTTGTTACAGCCGACAATCTAGCTTGTAAACCCTTCTGGAAGCTTGG    -   -	CAGCCAGCATGGCTGGGACATGCAGGTGTCCTTCGACCATGCACGCCCGCAC 	CCGFTTCTTCTTCTTCTACAAGCTCAAGCACGAAGGACCTTTCAAG 	STAAGCAGGAGCAACTACAGAGACGACCAGCTGCCTCCTTCAAAATGTT  -  -  -  -  -  -  -  -  -  -  -  -  -	ntatataattagactggtggatgacactaacacaacaagaaaagtgatg  :  -  -  -  -  -  -  -  -  -  -  -  -	AAAGCCATGGCACTCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATC	FGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCCGCAAGAA

1216 TGGGTNATHGARARATHCAYGARGARHSSNCARTTYATHATHGTNGTNTGTWSNAARGGNATG 1275 GACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCCTCAG 1645 TTCCATCCTCCTCCACTGCGCTACCGGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTG 1885 2126 TOGICIGIGOCCICAICCGAGCIGICICIGCCACIGAIGGAAGGACICICGACGGACCAG 2185 2186 ACAGAAACGTCTTCCCTGACGGAGAGCGTGTCCTCCTTCAGGCCTGGGTGAGGAA 2245 GAAAATATATTTCACATTTAGATGAGAGAGCTCTTGAGTCTTCCACATACACTGCAGCA TGGGTCATCCAGAAGATCCACGAGTCCCAGGTTCATCATTGTGTGTTCCAAAGGTATG GCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGGTCAGCATGGGGGC 1336. 1766. 

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2116; CÇNCCNGCNTROCNWSNAARTHYTNWSWRSNTGRAARGCNGAYYTNGGNTGY 2175
                      2056 ACNGARACHWSNWSNWTNACNGARWSNGTNWSNWSNWSNWGGNYTNGGNGARGARGAR 2115
                                                     2246 CCTCCTGCCCTTCCTTCCAAGCTCCTCTTCTGGGTCATGCAAAGCAGATCTTGGTTGC 2305
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13. 7. 2.1. ABA9503

ABA95038 standard; DNA; 2217 BP. (first entry) 20-MAY-2002 ABA95038;

Murine cytokine receptor, Zcytori8 degenerate coding sequence.

Cytokine receptor; 2cytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; mouse; ds.

Mus sp.

WO200208259-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US23253.

26-JUL-2000; 2000US-220747P.

(ZYMO ) ZYMOGENETICS INC.

Presnell SR, Kuestner RE,

Gao Z;

WPI; 2002-217048/27.

P-PSDB; ABB07630.

New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ligand

Disclosure; Page 118-119; 119pp; English.

The Invention relates to an isolated cytokine receptor polypeptide designated Ecytoria. The Ecytoria polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with polypeptides can be used to inhibit encoding nucleic acids are useful for providing Ecytoria in vivo by gene therapy techniques. Ecytoria oligonucieotide probes are useful for invivo diagnosia, and the Ecytoria probes and primers can be used to detect and localize Ecytoria gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Ecytoria gene resides. The Ecytoria polyuucieotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a murine Ecytoria degenerate coding sequence. \*\*\*\*\*\*\*\*\*\*\*\*\*

Sequence 2217 BP; 362 A; 236 C; 365 G; 289 T; 965 other;

.. 2 Best Local Similarity 51.7%; Pred. No. 0; Matches 1173; Conservative 549; Mismatches 485; Indels 60; Gaps 55.5%; Score 1322.4; DB 24; Length 2217; 51.7%; Pred. No. 0; Query Match

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GCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATCACAGTG 1042 1103 CAAGAAAATATATATTCACATTTAGATGAAGAGGCTCTGAGTCTTCCACATACACTGCA 1162 GCACTCCCAAGAGAGGCTCCGGCCGCGGCCGAAGGTCTTTCTCTGTTTCCAGTAAA 1222 622 682 558 CCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCCGCAAGAAGCAA, 1102 206. TGGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTGCTAATGAGGGAGTGGGGCCA 265 503 CAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATG 562 146 TCGCAGCTGCCTGTGCCGCTGCCGGTCCGGCCGCGCGCGGGGCGCCGACACCTGTGGC 205 121 TGGMG------NGGNGTNGGNCCN 138 266 GCCAGCAGAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTAC 325 139 GCNWSNWGNAAYWSNGGNYINCAYAAYATHACNTIYMGNTAYGAYAAYTGYACNACNTAY 198 383 TATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATC 442 GACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGCCTCGGAACCTG 742 863 ACCIGIAAGCAGGAGCAAACIACAGAGACGACCAGCIGCCICCTICAAAAIGTITCICCA 922 GGGGATTATATATTGAGCTGGTGGATGACACTAACACAACAAGAAAAGTGATGCATTAT 982 GINGINAARWSNGINCARWSNCCNTGGGCNGGNCCNATHMGNGCNGINGCNATHACNGIN 918 326 TTGAATCC --- AGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAG 382 619 AAYATHWSNCARCAYGGNWSNGAYATGCAYGTNWSNTTYGAYCAYGCNCCNCARAAYTTY 678 GGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGAACCTTTCATGAAGCGAAAG 862 9 1. ATGGCNCCNTGGYTNCARYTNTGYWSNTTTTTTTTACNGTNAAYGCNTGYYTNAAYGGN 443 GAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGGGAAGACAGTGC GAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAAAGGTTGTCCCT 623 TITCCTICCATTAAAAAGGAAAGCAATTACACCCTITCTITAGAACCCGAGCCIGI 263 439 683 803 923 859 1039 199 983 1043 919 979 윱 셤 ò a ö g g ð 쉄 ö ö g a à g ò

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1223 GATGGCCAGAATCACATGATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGT 1282
                                                                 ATGAAGTACTTGTGGACAAGAAGTACAAACACAAAGGAGGTGGCCGAGGCTCGGGG 1462
                                                                                                                                                                                                       1463 AAAGGAGGTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAG 1522
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               CAGAGTTCGTCCGCGCGCCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCCTGCGAG 1582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTIGCAACAIGCACCAGITIAIIGACGAGGAGCCCGACIGGIICGAAAAGCAGIICGII 1822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1933 CARCCNTINTINCAYGCNGINAARGCNGGNWSNCCNWSNGARAIGCCNMGNGAYWSNGGN 1992
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                                                   GGCTGTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGA
                                                                                                  GAÄTGGGTCATCCAGAAGATCCACGAGTCCCAGTTCATCATGTGGTTTGTTCCAAAGGT
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-infammactory; anti-dabetic; immunosuppressive; anti-introbial; hepatic; anorectic; immunosuppressive; anti-introbial; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; anti-convulsant; anti-leukeemic; anti-infertility; ophthalmological; hepatitis; anorexia; cacheria; neuronal, dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inappropriate IL-17 receptor like polypeptide (ILI/IIp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzhelmer's disease, Parkinson's disease and epilepsy), lung disgreers (e.g. cystic fibrosis, asthma and emphysema), skin disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypetides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-ashmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities: The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding interleukin 17 receptor like polypeptides, asselli for preventing, diagnosing and treating, e.g. Leukaemia, asthma, disheres, psoriasis and alaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotides
                                                                                                                                                                                                                                                                                                         Human interleukin 17 (hIL-1) receptor-like cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Figure 1 are missing in
2297 CTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCCTTT 2343
                                           2170 CAYGGNTGYCAYWSNCAYACNGAYGARYTNCARGCNYTNGCNCCNYT 2216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product- "hIL-17 receptor-like protein
/note- "Human interleukin 17"
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/note- "No start or stop codon given"
/transl_except- (pos:960, as Pro)
/note- "This codon is incomplete, as
961-3720 of Figure lare miss
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75..960
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diabetes, psoriasis and glaucoma
                                                                                                                                                                        AAS16201 standard; cDNA; 960 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2001; 2001WO-US08678.
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940 TGATGCATTATGCCTTAAAGC 960

ce.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemis), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. infertility and atherosclerosis, cancers (e.g. infertility and miscariases), expediences (e.g. infertility and miscariases), expendents (e.g. infertility and miscariases), expediences (e.g. infertility and and tastomatic between the prosence of similar nucleic adiasitic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The Illipip may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The expression and activity, This sequence encodes the 5 portion (bases 1.96) of human interleukin 17 (IL-17) receptor like protein described in the method of the invention. ö 252 AGGGAGTGGGGCCAGCCAGCAGAACAGTGGGCTGTACAACATCACCTTCAAATATGACA 311 312 ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCA 371 180 ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCA 339 372 CCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGG 431 491 GAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAA 611 731 852 TCAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGGACGACCAGCTGCCTCCTTCAAA 911 912 ATGTTCTCCAGGGATATATAATTGAGCTGGTGGATGACACTAACACAACAAGAAAG 971 880 AIGTITCICCAGGGAITATATAATIGAGCIGGIGGAIGACACTAACACAACAAGAAAG 939 GAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 551 732 CTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGCAGGTGTCCTTCGACCATGCAC 791 CGCACAACTICGGCTTCCGTTTCTTCTTCTTCACTACAAGCTCAAGCACGAAGGACCTT 851 Gaps CCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGG CCCGAGCCTGTGACCTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGC nucleotides 961-3720 are missing (for nucleotides 3721-4483; see AAS16202). ö 31.0%; Score 737.8; DB 23; Length 960; 1larity 99.7%; Pred. No. 3.9e-197; Conservative 0; Mismatches 2; Indels 0; Sequence 960 BP; 258 A; 234 C; 236 G; 232 T; 0 other; (e.g. eczema and psorlasis), kidney disease (e.g. bone diseases (e.g. osteoporosis and hypercalcam 972 TGATGCATTATGCCTTAAAGC 992 Best Local Similarity Matches 739; Conservat Query Match 00 552 672 792 99 33 192 220 셤 8888888888888888888 g õ 셤 ö 셤 셤 윱 ö 윤 ö 요 õ 윱 ò å 셤 ö 셤 ð 윰 ò

1236 ACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGTGGCTGTGAGGTGG 1295 1264 ACGIGGACGIGGACCTGAAATTCGCCCAGTCCTGCTCACCGCCTGCGCACGGAAGTGG 1323 1296 CTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAATGGGTCATCC 1355 AGAAGATCCACGAGTCCCAGTTC-----ATCATTGTGGTTTGTTCCAAAGGTA 1403 Gaps DNA encoding interleukin-17 receptor - useful for regulating immune and inflammatory responses, or to suppress graft rejection (IL-17R) (AAW04185), a type I transmembrane protein. It was isolated from a human peripheral blood lymphocyte library by screening with murine IL-17R DNA (see also AAW33800). The CDNA can be used to produce (pref. soluble) recombinant IL-17R in transformed host cells, or to transfect a tissue or organ to be transplanted as a means of suppressing graft rejection in the cDNA clone (AAT33801) codes for human interleukin-17 receptor Indels 12; Query Match 3.0%; Score 71.4; DB 17; Length 3223; Best Local Similarity 46.4%; Pred. No. 4e-09; Matches 280; Conservative 0; Mismatches 311; Indels 12; Interleukin-17 receptor; IL-178; autoimmune disease; allergy; asthma; graft rejection; inflammation; therapy; ss. Sequence 3223 BP; 635 A; 1034 C; 970 G; 584 T; 0 other; AAT33801 standard; cDNA to mRNA; 3223 BP; Human interleukin-17 receptor cDNA. Location/Qualifiers 93..2693 Claim 1; Page 37-41; 52pp; English. Fanslow WC, Spriggs MK, Yao Z; 95US-0538765. 95US-0410535. 96WO-US04018 93..173 /\*tag= b 174..2690 /\*tag= c (first entry) ø /\*tag= (IMMY) IMMUNEX CORP. WPI; 1996-443184/44. P-PSDB; AAW04185. - IV-80762909-A1: Homo sapiens 05-DEC-1996 21-MAR-1996; 07-AUG-1995; 23-MAR-1995; 26-SEP-1996. sig\_peptide mat\_peptide AAT33801; 1356 RESULT 15 ò 윰 ò đ ò

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a	1384 GT	1384 GTCAGAAGCAGGAGATGGTGGAGAGCAACTCTAAGATCATCGTCCTGTGCTCCCGCGGGCA 1443	1443	
δ	1404 TG	1404 TGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAAGGGGGGGG	1463	
g	1444 CG	1444 cécecechangreschagescherresseschessescherressescherescher 1503	1503	٠.
δ	1464 AA	AAGGAGGCCTCTCCTGGTGGGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAGC	1523	
a	1504 AC	AGGAAAGCCGTGGGGGACCTGTTCACTGCAGCCATGAACATGATCTCCCGGACTTCA	1563	
ò	1524 AG	AGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCCTGCGAGG	1583	
g	1564 AG	AGAGGCCAGCTTCGGCACCTACGTAGTCTGCTACTTCAGCGAGGTCAGTGTGAGG	1623	
δ	1584 GA	GACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCCTC	1643	
ą	1624 GC	1624 GCGACGTCCCCGACCTGTTCGGCGCGCGCGCGCGCGCTACCGCTTCGAGG	1683	
Ωy	1644 AG	1644 AGCTCTGTTCCCACTTGCACTCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGC	1703	
g	1684 AG	GIGTACTTCCCCATCCAGGACCTGGAGATGTTCCAGCCGGGCGGCATGCACCGCGTAG	1743	
δλ	1704 GA	CAGGGCAGCAGAAGTACTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCA	1763	
q	1744 GG	1744 GGGAGCTGTCGGGGGAACTACCTGCGGAGCCCGGGGGGGG	1803	
ď	1764 TT	TTTGCAACATGCACCAGTTTATTGACGAGGCCCGACTGGTTCGAAAAGCAGTTCGTTC	1823	
qq	1804 TG	TGGACAGGTICCGGGACTGGCAGGTCCGCTGTCCGGATCGATATGTGACAACCTCT	1863	
ογ	1824 CC	CCT 1826		
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Search completed: May 12, 2003, 21:13:08 Job time : 374 secs

. 2 13.6 577 12 BG721995 BG721995 .2 13.4 5680 10 BB263921 BB263921 .4 12.8 705 9 AL728651 AL728651	10 500.4 12.6 1010.14 20734807 12 260.8 10.9 813.13 BG985616	253 10.6 323 14, BQ306217: 247.4 10.4 526 12 BF615262 238 10.0 636 13 BG985614 237.4 10.0 448 10 BE679435	233.4 9.8 614 13 B1897186 B1887186 229.8 9.6 584 9 AL650928 AL650928 211.8 9.9 585 12 BG149830 BG149830 205. 8.6 659 10 BB616562 BR616562	204.8 8.6478 13 BJ039933 192.8 8.1541 10 ANG41445 189.2 7.9230 12 BF515598	24 184.2 - 7.7856 10 -88470523 B8470523 198464320 25 183.8 7.7 - \$45,-9 -AL777282 AL777282 AL777282 AL777282 25 172.8 AL777282 AL777	167.2 7.0 730 13.:B1887498 B1887498 161.4 6.8 411 10 AW767246 AW767246 150.6 6.3 698: 17 BH066762 BH066762 150.2 6.3 424 10 AW766603 AW766603	31 148.4 6.2 291c 10 BB288374 BB28874 BB268674 32 131 5.5 398 9 A1088588 A1088588 A1088588 A1088588 A1088588 A1088588 A1088588 A108858	35 121.4 5.1 494 10 AW233130 AW233130 36 119.0 5.0 633 13 BT888786 B1888786 37 117.4 4.9 596 14 BQ450554 BQ450554 38 103 4.3 806 14 BG4856577 BGGGK617	100 4.2 520 17 BH091008 BH091008 B9 3.7 563 13 BJ030747 BJ030747 BJ030747 BJ037093 B	Car to Tra	79 3.3 284 17 FR0016488 AL011364 F	ALIGNMENTS		ION BB616055 RIKEN full-length enriched, adult male test CDNA clone 4931403M23.5', mRNA sequence. ON BB616055	VERSION BB616055:1 GI:16456248 KEYMORDS EST SOURCE house mouse	Fuk Kam	. 15	aki, A., Nomura, K., Ohno, P akai, C., Sakai, K., Sano, B iraki, T., Sogabe, Y., Suzu	Auramatsu,M. and Hayashizaki,Y.  Huramatsu,M. and Hayashizaki,Y.  RIKEN Mouse ESTS (Arakawa,T., et al.  AL Unpublished (2001)	COMMENT Contact::Yoshihide Rayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences.Center(GSC), Yockbama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suchtro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9212 Fag: 81-45-503-9216
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: May 12, 2003, 10:35:26; Search time 2245 Seconds (Without alignments) 17191.022 Million cell updates/sec	Title: Perfect score: 2383 Sequence: 1 ccgccgcggccaccgccacaagcattgccactttagctg 2383	Scoring table: IDENTITY_NUC Gapext 1.0	16154066 seqs, 8097743376 residues	Total number of hits satisfying chosen parameters: 32308132 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database: EST:* 1: em_estha:* 2: em_esthum:*	3: em_estin:* 4: em_estuu:* 5: em_estou:* 6: em_estol:*	7: em_estro:* 8: em_htc:* 9: em_htc:*	10: 95_est2:* 11: 95_htc:*	12: gp_est3:* 13: gp_est4:* 14: gb_est5:*	15: em_estrun:* 16: em_estrun:* 17: gb_gss:*	·		44: em_gss_mus:* 25: em_gss_other:* 26: em_gss_pro:*	esults predicted by chance	and is derived by analysis of the total score distribution.  SUMMARIES	Result Query No. Score Match Length DB ID Description	1     453.6     19.0     649     10     BB641245     BB641245

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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 665)
Arakawa, T. Carnindi,P., Fukuda,S., Furuno,M., Hanagakh,T., Hara,A., Haramoto,K., Hori,F., Ishil,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Tkomita,R.; Ohno,H., Kouda,D., Shibata,K., Shinaki,T., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinaki,T., Shinaki,T., Sakai,K., Suo,H., Sasaki,D., Shibata,M., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Riken Mouse Ests (Arakawa,T., et al. 2001)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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Fmail: genome-reségsc.riken.go.10
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UNL.http://genome.gac.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Huramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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BB641245 GI:16476370
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                                                                                                                                         451 GAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGGGAAGACAGTGCCAACAACT 510
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Email: genome-resegsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp,
Carnincip., Shibata,Y., Hayatau,W., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramateu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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genes. Genome Res... 10 (10), 1617-1630 (2000)
Wadi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahik,M., Yoneda,Y., Ishikwa,T., Ozawa,K., Tanaka,T., Marsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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0; Mismatches 96; Indels 0;
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TCTTTGGTCCCCAGGGCCCTTGGCATTGAATTCCTAAAAGGATTCCGAGTCATCCTGGA 379
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                                                        Computer-based methods for the mouse full-length cDNA encyclopedia real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Rayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences: Mamm. Genome. 12, 673-677 (2001)
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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/clone="A830013G13"
/clone=llb="RIKEN full-length enriched, 10 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 CACCTTCAGATACGACAACTGTACCACCTACTTGAATCCCGGCGGGAAGCATGCGATTGC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 GCTTTGTGTTGCTAATGAGGGAGTGGGGCCAGCCAGCAGAACAGTGGGCTGTACAACAT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 TGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415 TCTTTGGTCCCCAGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 GAGAACGGCCTGGCCGAGCGCACGCCATGGCCCCGTGCCTGCAGCTCTGCTCCGT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GAGACCGGCCCAACTGGGCGAGCGTACGGCCATGGCCCCGTGGCTGCAGCTCTGCTCTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 CGGCCGCGCGCGCGCCCGACACCTGTGGCTGGAGGATGAAAGCGGCTGCCCGACCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 CACCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 18.2%; Score 433; DB 10; al Similarity 83.6%; Pred. No. 1.5e-102; 521; Conservative 0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 t
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 c
                                                                                                                                                                                                                                                                                                                                                                                                          mouse tissues
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Best Local S
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ORIGIN
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Email: smitheemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 547)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from day 20 and day 40
GGAGCTGAAGTCGGAGGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCT 534
                                       535 CAACAGTAGCTTCAAAAGAACTGGAATGGAATCTCAAACCTTTCCTGAATATGAAATTTGA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            201867-MARC 4BOV, Bos taurus CDNA 5', mRNA sequence.
BE750478
BE750478.1, GI:10164470
                                                                                                                                                                                                                                                                                                                                                                                                                             ira iinear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA v
Tel: 402, 762, 4366
Pax: 402 762, 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.1%; Score 431; DB 12;
86.1%; Pred. No. 4.5e-102;
tive 0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus" / db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                         547 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 112 row: C column: 10 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="MARC 4BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pooled.
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                                                                                                                                                                                                                                                                                                                               560 TCCCTTCTTCTGAACACGGG 582 ..
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                                                                                                                                                                                                                                                                                        655 CCCTTTCTTTAGAACCCGAG 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="
                                                                                                                                                                                                                                                                                                                                                                                                                     BE750478
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/dev_stage="19 weeks"
/lab_host="19 weeks"
/lab_host="19 weeks"
/lab_host="0410B (ampicillin resistant)*
/lab_host="041
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Bukaryota Wetzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to. 377)
Dias Neto, E., Garcia Correa, R., Verjovski Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G. H., Carvala, A. Fr., Natsukuma, A., Bala, G.S., Simpson, D. H.,
Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O' Hare,
M.J., Soores, P.; Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF803798 377 bp mRNA linear EST 12-JAN-2001
MRO-C10075-021100-003-c02 C10075 Homo sapiens cDNA, mRNA sequence.
BF803798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGTCATGTGCAAACCAGGGCCTGAGAGTGACTTCTGCCTAAAGGTAGAGGCGGCTGTT 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1955 CTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGAGTCAGCATGGGGGGCCTGGACCAA 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 CTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGAGTCAGCATGAGGGCCTGGACCAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 GACGGGGA-GCCGGCCTGCCCTTGACGCCCCCCTCCTGCTGCACG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2075 GTGAAAGCCGGCAGCCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTG 2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2195 TCTTCCCTGACGGAGAGCGTGTCCTCCTCTTCAGGCCTGGGTGAGGAGGAACCTCCTGCC 2254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 GTGAAAGCCGGCAGCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 GATGTCATGTGCAAACCAGGGCCTGAGAGTGACTTCTGCCTAAAGGTAGAGGCGGCTGTT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2015 GACGGGGGCCCGGCCTGCCCTTGACGGTAGCGCCGCCCTGCAGCCCCTGCTGCACACG
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llarity 99.2%; Pred. No. 1.2e-87;
Conservative 0; Mismatches 2; Indels 1;
             /db_xref="taxon:9606"
/clone="IMAGE:379623"
/clone_11b="Soares_fetal_heart_NDHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2255 CTTCCTTCCAAGCTCCTCTTCTGGGTCAT 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCCTTCCAAGCTCCTCTTCTGGGTCAT 1
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Best Local Simi
Matches 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
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AUTHORS
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BF803798
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2f42f08.sl Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone
IMAGE:279623 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bomo sapiens:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 390)
1 (bases 1 to 390)
1 (bases 2 to 390)
1 (bases 3 to 390)
2 (bases 3 to 390)
2 (bases 4 to 390)
3 (bases 4 to 390)
4 (bases 5 to 390)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40mij fwd. Er from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                               61. CGCCTGCCTCAACGGTTCGCAGCTGGCTGGCTGCAGGCGCTCCAGCAGAGCGCGGGGG 120
                                                                                                                                                                                                                                                                                                                                                   CGCCGACACCTGTGGCTGGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTTGCTAA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 GGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                   1. GGGCGAGCGCACGCCATGGCCCCGTGGCTGCAGCTCTGCTCGGTCTTCACGGTCAA
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314,286 1810
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/db_xref="GDB:1287879"
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human.

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

source

FEATURES

RESULT 4
AA778029/c
LOCUS
DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

499

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Blackshear, P.J.; IdliW.S.; Thorn, J.M., Kennington, E.A.; Staffa, N.G. Jr., Moore, D.T.; Bouffard, G.G.; Beckstrom-Sternberg, S.M.; Touchman, J.W.; Bonaldo: M.F. and Soarea, M.B.
The NIEHS Xenopus maternal EST project: Interim analysis of the first 13,879-ESTs from unfertilized eggs.

21211403
                                                                                                                                                                                                                                                               Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
Office of Clinical Research and Laboratory of Signal Transduction
National Institute Environmental Health Sciences
A2:05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: black009@nlehs.nih.gov
clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC).
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_llb ** Blackshear / Soares normalized Xenopus egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type-"unfertilized egg"
/cell_type-"unfertilized egg"
/dev_stage-"unfertilized egg"
/lab_host-"DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .627
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="PBX0153F07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: TGTAAAACGACGGCCAGT
HACKWARD: CAGGAAACAGCTATGACC
Plate: 0153 row: F column:: 07
Seq primer: T7 primer.
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Best Local Similarity 70.3%;
Matches 436; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Tel: 919 541-4899
Fax: 919 541-4571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ibrary
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                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: asimpson@ludwig.org.br.
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethiml2.pl?tl-MR0&t2-MR0-C10075-051100.003-co565t5-2000-11.02st4-1)
Seq primer: puc.18 forward
High quality sequence stop: 377.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: colon_ins; Vector: pucl8; Site_1: Smal;
Site_2: Smal A mini-library was made by cloning products
derived from ORESTES POR (U.S. Letters Patent application
No. 196,716 - Ludwig institute for Cancer Research)
profiles into the pucl 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1011 CCGGGCCCATCAGAGCCGTGGCCATCACAGTGCTACTGATATCGGCATTCGCGA 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1191 GGCCGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGCCAGAATCACATGAATGT 1245
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5a-81; Indels 0;
                           ce rags
Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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ilarity 99.4%; Pred. No. 2.5e
Conservative 0; Mismatches
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/db_xref-"taxon:9606"
/clone_lib-"C10075"
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                                                                                     Contact: Simpson A.J.G.
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AW645591.1 GI:7403045
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Xenopus laevis
                                                                                                                                                                                                                   rel: +55-11-2704922
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Matches 353;
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Anote-"Vector: pTTT3-Pac; Site_1: ECORI; Site_2: NotI; POlyA-selected mRNA was prepared from unfertilized Xenopus laevis egg. The library was constructed in the vector pTTT3-Pac as described in Bonaldo, M.F., Lennon, G. and Soarse, M.B. Normalization and subtraction: .two approaches to facilitate gene and subtraction: .two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dTIB primer; double stranded colbas were ligated to ECORI adapters, dilested with NotI, and directionally cloned into:the NotI and ECORI-digested pT7T3-Pac vector. The library contained approximately 7.2 % 10.5 recombinants, with average insert sizes of 1-1.5 kb.*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 TGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 AGCAGAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 AATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCT 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 627;
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Pred. No. 2.6e-74;
0; Mismatches 184; Indels
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E 1 (bases 1 to 577)
S WIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

D NIH-MGC http://mgc.ncl.nih.gov/.

Contact; Robert Strausberg, Ph.D.

Contact; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG721995. 577 bp mRNA linear EST 08-MAY-2001 602698761F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4830807 5',
                                          749 AGCCAGCATGCCTCGGACATGCAGGTGTCCTTCGACCATGCACCGCACACTTCGGCTTC .808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 ITGITGCAGCCGGACAGTCTGACCTGCAGGCCATACTGGAAACCAAAAAACGTCAGCGTC 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 AACTCTTATTCCGTCAACTACAAACTGAAGGCGCGCTCCTTTAAACAGAAGATCTGC 602
: . 509. CTGATTCTAAAGGATCCGAAGAGTCAACAGTAGCTTCAAAAGAACTGGAATGTAATCT
                                                                                                                                                                                                                                                                                                                                                                                                       689 TIGITACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAÄGCCTCGGAACCTGAACATC
                                                                                                                                           CAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAAAGGTTGTCCCTTTTTCCT
                                                                                                                                                                                                                                                                                       TCCATTAAAAACGAAAGCAATTACCACCCTTTCTTTTAGAACCCGAGCCTGTGACCTG
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/clone_lib="NIH_MGC_97"
/lab host="nuff"
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8G721995
8G721995.1 GI:14001182
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

RESULT 7 BG721995

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source

FEATURES

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Mus musculus
Budaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Murinae; Mus.
1 (bases 1 to 680)
1 (bases 1 to 680)
1 (bases 2 to 680)
1 (bases 3 to 680)
1 (bases 4 to 680)
1 (bases 5 to 680)
1 (bases 6 to 680)
1 (bases 6 to 680)
1 (bases 7 to Carninothe, Futuno, M., Mawai, J., Konno, H., Huramoto, K., Horti, F., Ishili, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Sasaki, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakwa, T., et al. 2001)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB263921 RIKEN full-length enriched, 10 days neonate cortex Mus musculus cDNA clone AB30013G13 3', mRNA sequence.
BB263921. GI:16400169
                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 TIGCCAIGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATCGAATT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGAAA-GGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGGGAAGACAGTGCCAAC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 TIGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATCGAATT 435
                                                                                                                                                                                                                                                                                                                           208 GAGGAIGAAAGCGGCIGCCCGACCCCGGCTIIGIGIIGCIAAIGAGGGAGIGGGGCCAGC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGC 387
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                          Query Match 13.6%; Score 325.2; DB 12; Length 577; Best Local Similarity 92.4%; Pred. No. 3.2e-74; Matches 353; Conservative 0; Mismatches 28; Indels 1;
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URL:http://genome.gsc.r1ken.go.jp/
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                                                                                                                                                  prepare full length cDNA, libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fullwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="cortex"
/dev_stage="10 days neonate"
/dev_stage="10 days neonate"
/dev_stage="10 days neonate"
/note="Site=1" Sall; Site_2: BamHI; cDNA library was
/note="Site=1" Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGACCAAGAGCTCTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A830013G13"
/clone_lib="RIKEN full-length enriched, 10 days neonate cortex"
Normalization and subtraction of captrapper selected CDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GGGAAGCATGCGATTGCTGATGCTCAGAACATCACCATCAGCCAGTACGCTTGCCACGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 GGGAAGCATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGAC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 CAGGTGGCAGTCACCATTCTTTGGTCCNCAGGGGCCCTTGGCATTGAATTCCTAAAAGGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 AGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGTG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 CAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTCCTGAAAGGA 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.4%; Score 318.2; DB 10; Length 680; 88.8%; Pred, No. 2.4e-72; Live 0; Mismatches 44; Indels 1;
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EST 18-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 705) (Colmbrack, Wellsen, Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Welssembach, and Petit, C. A subtracted cDNA, library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Danio rerio embryonic_inner_ear_subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    945 TGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCC 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1005 CGTGGGCCGGGCCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCAT 1064
                       inner ear subtracted cDNA Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 CGTGGGCCGGGCCGATCCGTGCCATGGCCATCACCGTCCGCTGGTCATGTCAGCCT, 262
                                                                       518 AAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTC, 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825 ACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAGCAGGAGCAAACTA, 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITCGGGTAATACTGGAGGAGCTGAAGICGGAGGGAAGACAGTGCCAACAACTGATTCTA 517
                                                                                                                                                                                                                  CTGAATATGAAATTTGAGACGGATTACTTTGTAAAGATTGTCCCTTCCCTTCCATTAAA 359
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                                                                                                                                                                        Query Match 12.8%; Score 304.4; DB 9; Length 705; Best Local Similarity 68.3%; Pred. No. 1.1e-68; Matches 422; Conservative 0; Mismatches 196; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 ACTACAAACTCAGAACGGAAGGACCGTTCAGACTCAAGCGTGCAAACCTGAGCAAACG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope ; Centre National de Sequencage BP 191 91006 EVRY cedex - Prance Email: seqrefêgenoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                 AL728651 Danio rerio embryonic inner ear subtract
rerio cona clone BNOAA1002B10 3', mRNA sequence.
                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="embryonic"
/note="subtracted cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                705 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL728651.1 GI:20193255
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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AL728651
LOCUS
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KEYWORDS
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/lab_host="bill0B (phage-resistant)"
/note="Organ: whole embryo; Vector: pcWV-SPORT6; Site_1:
NotI; Site_2: Sall; Cloned unddirectionally. Primer: Oligo
dT. Average insert size 2.1 kb. Constructed by Life
// Constructed by Life
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AGENCOORT_8510861 NICHD XGC Emb4 Xenopus laevis cDNA clone INAGE-664214 5', mRNA sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Biosocience Corporation
Clone distribution: NCT-CGPA clone distribution information can be
found through the I.M.A.G.E. Consortium/Linl at:
www-blo.linl.gov/bbrp/image/image.html
Plate: LIAM1056B row: m column: 15
High quality sequence stop: 428.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Kenopus Gene Collection (XGC
1 library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                    1125 TAGATGAAGAGGCTCTGAGTCTTCCAGATACACTGCAGCACTCCCAAGAGAGGCTCC 1184
                                                                                                                                                                     1185 GGCGCGCGCAAGGTCTTCTCTGCTATTCCAGTAAGATGGCCAGAATCACATGAATG 1244
                                                                                                                                                                                                                                                 1245 TGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGTGGGTGTGGTGGCTCTGGACC 1304
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1305 TGTGGGAAGACTTCAGCCTCTGTAGAAGGGCAGAGAGAATGGGTCATCCAGAAGATCC 1364
                                    123 TGGACGAGAGAGCTCGGAGTCTTCATCGCAGACCACGGCTCTGAGCGCAGACCACGACCT 382
                                                                                                                                                                                                     383 GGCCCAGACCCAAAATCTTCATCTGTACTCCAGCAGAGGGAGCCAAACACCTCGCC 442
                                                                                                                                                                                                                                                                                   clone_11b-"NICHD XGC Emb4"
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db_xref-"taxon:8355"
clone-"IMAGE:4684214"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Igor Dawid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BO734807.1 GI:21873704
EST.
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Unpublished (1997)
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cmowols/
cmc5c05.wl Blackshear/Soares normalized Xenopus egg library Xenopus
laevis cDNA clone PBX0161E05 5', mRNA sequence.
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1 (bases: 1 to 485)

1 (bases: 1 to 485)

1 Blackshear, P. J. Lal, W.S., Thorn, J.H., Kennington, E.A., Staffa, N.G.

1 Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.H., Touchman, J.H., Bonaldo, M.F. and Soares, M.J.

The NIEHS Xenopus maternal EST project: Interim analysis of the first 13,879 ESTS from unfertilized eggs

Gene 267 (1), 71-87 (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Office of Clinical Research and Laboratory of Signal Transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1304 CTGTGGGAAGACTTCAGCCTCTGTAGAGAGGGCAGAGAGAATGGGT--CATCCAGAAGA 1361
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                                                                                                                                                                                                                                                                                                                                                                                       945 TGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCC, 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1005 CGTGGGCCGGCCCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCAT 1064
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                                                                                                                                  825 ACTACAAGCICAAGCACGAAGGACCITICAAGCGAAAGACCIGIAAAGCAGGAGCAAACIA 884
                                                                           4; Gaps
                                                                                                                                                                                             19 ACTACAAACTGAAGCACGAGGCTCCTTTAAACAGAAGATCTGCCGGAAGGTGCTGAACA 78
                                                                                                                                                                                                                                                              885.CAGAGACGACCAGCTGCCTTCAAAATGTTTCTCCAGGGGATTATATAATTGAGCTGG
Query Match
Best Local Similarity 70.5%; Pred. No. 1.5e-67;
Matches 443; Conservative 0; Mismatches 181; Indels 4;
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mRNA sequence.
BG985616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: p1713-Pac, Site_1: EcoRI; Site_2: NotI; PolyA-selected_mRNA was prepared from unfertilized Xenopus
                                     National institute of Environmental Health Sciences A2-05 NIEBS: 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Research
                                                               Tel: 919 541-4899

Fax: 919 541-4899

Fax: 919 544-571

Email: black1095ales.nih:gov
Clone is available:through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsvaller, AL-35901

Phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
Ona connection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taevis eggs. The library was constructed in the vector privat-page as described in Bonaldo, M.F., Lennon, G and Soares, M.B. wormalization and subtraction: two approaches to facilitate gene discovery', Genome Researce 5.791-806, 1996. The first strand synthesis used a NotI-driB primer; doubles stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested private vector. The library contained approximately 7.2 x 10.5 recombleants, with average insert sizes of 1-1.5 kb."
                                                                                                                                                                                                                                           Counterbyeur. Com
DNA Sequencing and analyses performed by National Institutes of
Health Intramural Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 CTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAATCT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 AGCAGAAACAGTGGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 TGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 629 TCCATTAAAAACGAAAGCAATTACCACCTTTCTTTTAGAACCCGAGCCTGTGACCTG 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 AATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGGGAAGACAGTGCCAACAA '508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569 CAACCITICCIGAATAIGAAAITIGAAACGGATTAITICGIAAAGGIIGICCCTITICCI 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 AGCAAGACACGGGGTGCCCAATGTCACGTTACGATATGACAACTGCACTGCTTCATG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.0%; Score 263; DB 10; Length 485;
1larity 72.4%; Pred. No. 6.6e-58;
Conservative 0; Mismatches 130; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
                                   National Institute of Environmental
                                                                                                                                                                                                                                                                                                                                                                                                                             1. .485
/organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                      BACKWARD: CAGGAAACAGCTATGACC
Plate: 0161 row: E column: 05
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FORWARD: TGTAAAACGACGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: 17
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              BG985616 813 bp mRNA linear EST 13-JUN-2001 5059fl NICHD Zebrafish normalized I Danjo rerio cDNA clone 5059,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SuperScriptII reverse-transcriptage and tagged oligo-dr
primer which contains several restriction sites including
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/note="Vector: pBluescript KS+; Site_1: Not1; Site_2: Sal
; RNA was reverse-transcribed to first strand cDNA using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 947 GATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCCCG 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Molecular Genetics
National Institute of Child Health and Human Development, NIH
Bldg.6B, Room 413, 9000 Rockville Pike, Bethesda, MD 20892 USA
66 TGGGCGGGCCGATCGGTGCCATGCCATCACCGTCCGCTGGTCATGTCATGTCATCTTC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyprinidae: Danio.

1. (bases 1 to 813)

Kudoh, T., Tsang, M., Hukriede, N.A., Chen, X., Dedeklan, M., C.J., Klang, A., Schultz, S., Epstein, J.A., Toyama, R. and A gene expression screen in zebrafish embryogenesis Genome Res. 11 (12), 1979-1987 (2001)
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                                                                                                                                                                      435 TIGITGCAGCCGGACAGTCTGACCTGCAGGCCATACTGGAAACCAAAAAAC 485
                                                                                                           .689 TIGITACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGCCTCGGAAC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5059" :::
                                                                                                                                                                                                                                                                                                                                                                                                                               BG985616.1 GI:14389696
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193 g
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BF615262
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1 (bases 1 to 323)

1 (bases 1 to 323)

1 (bases 1 to 323)

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BQ306217
EST. GI:20837382
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-HR0st2-MR0-BT2003-050601-006-b08st3-2001-06-05st4-1)
Seq primer: pur 18 forward 52
High quality sequence start: 52
High quality sequence stop: 305
Location/Qualiflers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                       1187 CCGCGCCGAAGGTCTTCTCTGCTATTCCAGTAAAGATGGCCAGAATCACATGAATGTC 1246
1127 GATGAAGAGGTCTTGAGTCTTCCACATACACTGCAGCACTCCCAAGAGGAGGGCTCCGG 1186
                                                                                                                                                                                                                                                                                                            1247 GTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGTGGCTGTGGAGGTGGCTCTGGACCTG 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1367 GAGTCCCAGTTCATCATTGTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAG 1426
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2000: Watl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020: Sci. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Coganiam"Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="8972003"
/dev_stage="Adult"
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Waterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
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Library normalized by Jihwan Song
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
This clone is available royalty-free through LiML; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibbo
High quality sequence stop:
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Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2236 TGAGGAGGAACCTCCTGCCTTCCTTCCAAGCTCCTCTTTCTGGGTCATGCAAAGCAGA 2295
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2176
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/clone_lib="Xenopus laevis gastrula non normalized"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2117 ATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTCTCTGCCACTGATGGAAGGACTCTCG
                                                                                                                                                                                      Query Match. 10.6%; Score 253; DB 14; Length 323; Best Local Similarity 97.5%; Pred. No. 2.2e-55; Matches 278; Conservative 0; Mismatches 5; Indels 2;
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. L.
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                stringency conditions."
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Contact: Sandy Clifton, Ph.D.
                                                                                                112 g
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BF615262.1 GI:11788690
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Xenopus laevis
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gactagttctagatcgcgatcgcgacGGCGCcctttttttttttttttt. Second strand DNA was synthesized by E. coli DNA polymerase I in combination with E. coli RNAse H and E. coli DNA ilgase. Double stranded cDNA was ligated with Sali adapter. These CDNAs were cloned into the Sali/Noti site of pBluescript KS+ and transformed into E. coli Electromax DH10B by
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="bud to 10 somite stage embryos"
//dev_stage="bud to 10 somite stage embryos"
//note="vector: pBluescript KS+; Site_1: Not1; Site_2: Sal1
// RNA was reverse-transcribed to first strand cDNA using
SuperScriptII reverse-transcriptase and tagged oligo-dT
primer which contains several restriction sites including
a Not1 site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  607 CGTAAAGGTTGTCCCTTTTCCTTCCATTAAAAACGAAAGTAACAACTTTCTT 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            667 TAGAACCCGAGCCTGTGACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTG 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 CAAAACCATCAGGATGAGCTCACAGCCCTTCTCAAGTCTCGGCCTTCGAGACCGATTACAT 65
                                                                                                                                                                    Laboratory of Molecular Genetics
National Institute of Child Health and Human Development, N
Bidg.6B, Room 413, 9000 Rockville Pike, Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  907 TCAAAATGTTTCTCCAGGGGATTATAATTGAGCTGGTGGATGACACTAACAAGAG
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                   10.0%; Score 238; DB 13; Length 636; llarity 63.5%; Pred. No. 2.9e-51; Conservative 0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib-"NICHD Zebrafish normalized I"
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                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                           21588053
Other_ESTs: 5059t7,5059f1,5059r1
Contact: Dawld IB
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                  Bidg.6B, Room 413, 900
Tel: 301 496 4448
Fax: 301 496 0243
Email: idawidenih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone-"5059"
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Matches 396;
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                                                         TITLE
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COMMENT
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AUTHORS
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           /note-Vector: pBilasscript SK-; Site_1: EcoRI; Site_2:
Xhoi; cDRN was prepared from 2ug of poly A+ RNA (equal
parts from stage 10.5 and stage 11.5 gastrulae).
ECORI-Xhoi cut cDRN was then ligated into Unizap-XR
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
from the original library and normalized by hybridization
ECN to Cot-omega of 11. After removal of hybrids and
excess driver by streptavidin sepharose chromatography,
the ss-phagemids were made double stranded and
electroporated into Top-10 F'. Original library
contruction by Bruce Blumberg (Cho et al. 1991 Cell 67,
111-1120). Note: This is a Amnopus Gene Collection (XGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG985614 636 bp mRNA linear EST 13-JUN-2001 5059t3 NICHD Zebrafish normalized I Danio rerio cDNA clone 5059, mRNA sequence. BG985614 BG985614 GI:14389694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Danio rerio
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi,
Actinopterygii, Neopterygii, Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 GGGCCTCGGCATCGAATTCCTGAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TGCAAAATTGTGCCATTTCCCTCGCCAGAAATGAAAGTAATTACCATCCTTCTTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAG--TAGCTT 546
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 526;
                                                                                                                                                                                                                                                                                                                                                1 others
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Pred. No. 8.8e-54;
0; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; I
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/lab_host-"Top-10 F'"
                                                                                                                                                                                                                                                                                                                                                   123 g
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Best Local Similarity 68.9%;
Matches 353; Conservative
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BG985614
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Search completed: May 12, 2003, 21:03:57 Job time: 2258 secs

Scoring table:

Database :

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Mouse interleukin-
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N-PSDB; ABA95031, ABA95032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208259-A2.
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Human cytokine rec
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2333.435 Million cell updates/sec
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                                                                                                                                                                                              Description
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:
                                                                                                                  Run on: May 6, 2003, 13:34:21 ; search time 43 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseg/genesegp-embl/AA198
/SIDS2/gcgdata/geneseg/genesegp-embl/AA198
/SIDS2/gcgdata/geneseg/genesegp-embl/AA198
GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
                                                                             OM protein protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                  Searched: | 908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match
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New cytokine receptor polypeptide designated zcytor18, useful for Inhibiting cell proliferation associated with psoriasis or tumor

Human Interleukin

Human

Score

Result

The invention relates to an isolated cytokine receptor polypeptide designated Zcytoris The Zcytoris polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing zcytoris in vivo by gene therapy techniques. Exptoris oliponucleonide probes are useful for in vivo diagnosis, and the Zcytoris probes and primers can be used to detect and localize Zcytoris quesa xaberrations in chomosomes. The probes are also useful for detecting gross xaberrations in chomosomes in which Ecytoris gene resides. The Zcytoris polynuclegatides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytoris amino acid sequence. endogenous zcytor18 growth, and modulating immune system by binding to Claim 1; Page 2; 119pp; English.; 

753 AA; Sequence

PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240. 61 ASRNSGLÝNITFRÝDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120 61 ASRNSGLYNITERKYDNCTTYLNPYGKHYIADAQNITISQYACHDQYAVTLMSPGALGIE 120 FRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360 LPRERLRPRPRVFLCYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTR 540 OGSRRNYFRSKSGRSLYVAICNNHOFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660 121 FLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 720 1 MAPWIQICSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRICVANEGVGP 60 0; Gaps Query Match
100.0%; Score 4013; DB 23; Length 753;
Best Local Similarity, 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; 181 181 241 302 301 421 421 541 661 361 361 181 ò 셤 à 셤 ö 윱 à 셤 õ 셤 à g 8 ö g ð à a 윰

The invention relates to an isolated cytokine receptor polypeptide designated Scytoria, The Scytoria polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psortials or tumour growth. The encoding nucleic acids are useful for providing Scytoria in vivo by gene therapy techniques. Scytoria oligonucleotide probes are useful for in vivo diagnosis, and the Scytoria probes and primers can be used to detect and localize Scytoria gene expression in tissue asmiles. The probes are also useful for detecting gross aberrations in chromosome 3 in which scytoria gene resides. The Scytoria polygnucleotides can also be used in linkage-based testing of pulmonary alvoolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a

Disclosure; Page 94-98; 119pp; English.

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Gaps

Indels,

DB 23; Length 753;

99.8%; Score 4003; I 99.7%; Pred. No. 0; 11ve 0; Mismatches

Conservative

Similarity

Query Match Best Local Simi Matches 751;

Sequence

numan 2 cytor18 variant amino acid sequence.

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New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with peortasis or tumor growth, and modulating immune system by binding to endogenous zcytori8
                                                                                                                                                                                                           Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; huma pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; variant.
                                                                                                                                                                                                                                                                                                        /label- 7269M
/note- "wild-type Thr is replaced with Met"
Misc-difference 750
                                                                                                                                                                                                                                                                                                                                                              /label- V750A
/note- "wild-type Val is replaced with Ala"
                                                                                                                                                                                 Human cytokine receptor, Zcytori8 variant sequence.
Location/Qualifiers
                                                                                                ABB07627 standard; Protein; 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-217048/27,
N-PSDB; ABA95033, ABA95034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2000; 2000US-220747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-2001; 2001WO-US23253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Presnell SR, Kuestner RE,
                                                                                                                                                       20-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                          40200208259-A2
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                           ABB07627;
                   : <u>d</u>
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New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18

Claim 1; Page 102-106; 119pp; English.

ligand

23-JUL-2001; 2001WO-US23253. 26-JUL-2000; 2000US-220747P

Presnell SR, Kuestner RE, WPI; 2002-217048/27: N-PSDB; ABA95035, ABA95036.

(ZYMO ) ZYMOGENETICS INC.

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                                                                                                                                                                                                                              LPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGGRE 420
               9
                                                                                                                                                                 LHTVRAGSPSDWPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE
                        61 ASRNSGLYNITERYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSPGALGIE
                                                                                             SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR
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             1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP
                                                                                   PLEGPRVILEELESEGROCOOLILEDPROLNSSFERFIGMESOPPLINMKFETDYFVKVVPF
                                                                                                                      PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG
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Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
                                                                                                                                                                     cytokine receptor, Zcytori8 splice variant.
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            WO200208259-A2
                                                                                                            20-MAY-2002
                                                                                                                                                                                                                                                                                                                                     Homo saplens
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ABB07628
                                                         ABB07628;
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Human

RESULT

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The invention relates to an isolated cytokine receptor polypeptide designated Expressed by standard recombinant methodology. The polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with poorlasis or tumour growth. The encoding nucleic acids are useful for providing Scytorial in vivo by gene therapy techniques. Exptorial goligonucleotide probes are useful for in vivo diagnosis, and the Zcytorial probes and primers can be used to detect and localize Zcytorial gone expression in tissue asmiples. The probes are also useful for detecting gross aberrations in chromosome 3 in which inkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with pulmonary and erythroleukemia associated with human applymorphisms of cytokine receptors. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.1%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSIKNESNYHPFFFRTRACDLLLOPDNLACKPFWKPRNLNISOHGSDMOVSFDHAPHNFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human zcytor18 splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence. 739 AA;
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receptor like polypeptides useful as vaccines and in gene therapy. These have immunoadulatory, anti-inflammatory, anti-diabetic, anti-microbial, anti-parkhosonian, anti-inflammatory, anti-diabetic, anti-microbial, anti-parkhosonian, anti-covulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and ophthalmological activities: The IL-17 receptor like nucletc acids and proteins may be used to prevent and treat diseases associated with include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicamnia), weight disorders (e.g. anorexia, and obesity), neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-arbahaers; anti-convulsant; anti-asthaetic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes novel nucleic acids encoding interleukin (IL) 17
                                                                                                                                                     Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma
                                                                                                                              646
                                                                586
                                                                                                 660
                    lung disease;
                                                                                            601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL
467 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis; anorexis; cachexis; neuronal dysfunction; lung dis
bone disease; vascular disorder; eye disorder; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human Interleukin 17 (hiL-17) receptor like protein.
                                                                                                                                                                                                                   721 PPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 753
                                                                                                                                                                                                                                     Claim 2; Page 152-154; 158pp; English,
                                                                                                                                                                                                                                                                                                                             AAU09904 standard; Protein; 738 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2001; 2001WO-US08678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-2000; 2000US-189816P.
28-NOV-2000; 2000US-0724460.
                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2002 (first entry)
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N-PSDB; AAS15346.
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dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaenia), vascular disorders (e.g. stroke and atheroscierosis, cancers (e.g. leukėmia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therepy. The ILITrip may also be used as antigens in the production of antibodies against the proteins and in
                                                                                                                                                                                                                          assays to identify modulators of expression and activity. The anti-Lilrip antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human interleukin 17 (IL-17) receptor like protein described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPRERLRPRPRVFLCYSSKDGONHMNVVOCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 | HILLI | HAPWLOLCSVEFTVNACLNGSQLAVAAGGSGRAMGVDTCGWR------GVGP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISOHGSDMQVSFDHAPHNFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL
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                                                                                                                                                                                                                                                                                                                                              738 AA;
                                                                                                                                                                                                                                                                                                           the invention.
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PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 752

721

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1920 O. O. O. O.

9:707 PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 738

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# AAU09953 standard, Protein, 738 AA

AAU09953;

14-FEB-2002 (first entry)

Interleukin 17; hIL-17 receptor like protein immunomodulatory; anti-inflammatory; anti-diabetic; immunosupplessive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheumer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; cape disorder; mutant; mutant; Human Interleukin 17 (hiL-17), receptor like protein substitution #3. mutein. 

## Homo sapiens. Synthetic.

Misc-difference 363

/label- Ser, Thr, Ala, Cys

## WO200168859-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-US08678.

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC.

Jing S;

PI; 2001-611392/70.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psorlasis and glaucoma 

## claim 20; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These
have immunomidulatory, anti-inflammatory, anti-diabelic, anti-inforbial,
have immunomodulatory, anti-inflammatory, anti-diabeliaer's, renal,
anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
costeopathic, vascular, cytostatic, anti-leukemic; anti-infertility and
optional activities. The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat diseases associated with
inappropriate IL-17 receptor like polypeptide (ILI/TIP) expression. These
include, for example immune disorders (e.g. inflammation, diabetes and
cransplant rejection), infections (e.g. hepatitis and septicemia),
weight disorders (e.g. anorexia, cachexia and obesity), neuronal
cystuction (e.g. alzheimer's disease, parkinson's disease and epilepsy),
lung disorders (e.g. oystic fibrosis, asthma and emphysema), skin disease
(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
ce dystact cancer), reproductive disorders (e.g. infermility and
considerate and atherosocias and hypercalcaemia), vascular disorders
ce stroke and atherosocias and hypercalcaemia), vascular disorders
ce stroke and etherosocias and hypercalcaemia, myeloma and
chreat cancer), reproductive disorders (e.g. infermility and
considers needing restorative therapy. The ILI/Tip may also be used as
cutients needing restorative therapy. The ILI/Tip may also be used as
antigens in the production of antibodies against the proteins and in

AAU09954 standard; Protein; 738 AA.

RESULT 6

14-FEB-2002 (first entry)

AAU09954;

AAU09954 ID AAU( XX AC AAU XX DT 14-

ï assays to identify modulators of expression and activity. The anti-ILI7rlp antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human: Interleukin 17:(ILI-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 20. PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240 241 FRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA.300 661 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 720 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360 QCSRRNYFRSKSGRSLYVAICNMHOFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600 61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120 FLKGFRVILEELKSEGROCOOLILKDPKOLNSSFRRTGMESOPFLNMKFETDYFVKVVPF 180 LPRERLRPRPRVFICYSSKDGONHMWVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480 Indels 14; Gaps MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL Ouery Match 97.1%; Score 3897; DB 22; Length 738; Best Local Similarity 97.5%; Pred. No. 0; Matches 733; Conservative 1; Mismatches 4; Indels 14. 721 PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 752 738 AA; Sequence 47 181 301 347 121 541 707 227 287 107 181 467 527 601 8888888 ö g å 셤 셤 셤 à 윰 ;

7 7 7

Sequence 

Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; aiti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunctioh; lung disease; disease; vascular disorder; eye disorder; cancer; human; mutant; Human Interleukin 17 (hIL-17) receptor like protein substitution #4 . 3 G mutein. eucc

Homo sapiens.

· Location/Qualiflers Misc-difference 374

/label- val, Ile, Met, Leu, Phe, Ala, Nle

W0200168859-A2

20-SEP-2001.

15-MAR-2001; 2001WO-US08678

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC.

Jing S;

WPI; 2001-611392/70;

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma

Claim 21; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory cannot anti-inflammatory constant anti-inflammatory constantic, demandiogical, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate [L-17 receptor like polypeptide (IL)7 receptor li transplant rejection; infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. Alzheimer's disease, parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. sateoporosis and hypercalcemaia), vascular disorders (e.g. stroke and atheroscierosis, cancers (e.g. leukemia, myeloma and miscarriage), eyd disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as disquestic probes to detect and quantitate the presence of similar nucleic acids in samples and identify Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 21 anti-IL17rlp antibodies and antagonists may also be used to down regulate patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in and activity assays to identify modulators of expression expression and activity. antigens in the

738 AA;

Query Match

540 61. ASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120 FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFRRTGMESQPFLNMKFETDYFVKVVPF 180 181 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480 99 FRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360 QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE 720 1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60 14; Gaps SSSAALSKFIAVYFDYSCEGDVPG1LDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL Pred. No. 0; ; Mismatches 707 PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 738 PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 752 AAU09951 standard; Protein; 738 AA (first entry) Conservative Similarity 14-FEB-2002 AAU09951; Local Best Loca Matches 47 121 167 241 301 287 347 467 541 527 587 661 647 721 361 421 481 601 RESULT 7 AAU09951 ö 셤 ò 셤 8 음 ò 셤 à 셤 à 셤 õ g g ö 윱 ð 8 ŏ 윱 à 음 ŏ 셤 

97.1%; Score 3896; DB 22; Length 738;

Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-idabetic; immunosuppressive; anti-incrobial; hepatic; anabolic; ancrectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-inferility; ophthalmological; hepatitis; anorexia; cachezia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;

Human Interleukin 17 (hIL-17) receptor like protein substitution #1.

PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240 

181

167

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227 301 287 361 347 421 407 481

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The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-iablefic, intenal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascillar, cytostatic, anti-iablemers's inti-iableficial, or scallar, cytostatic, anti-iablemers' anti-iableficial, or ophthalmological activities. The IL-17 receptor like nucleic acids and protains may, be used to provent and treat diseases associated with insplant rejection; lee polypeptide (IL) the) expression. These include, for example immune disorders (e.g. inflammation, diabetes and risaplant rejection), infections (e.g. inflammation, diabetes and dysfunction (e.g. Alzhehmer's disease, Parkinson's disease and epilepsy), using disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g.; glomerulonephritis), bone diseases (e.g. cystic fibrosis, asthma and emphysema), vascular disorders (e.g. stroke and abebroscierosis, cancers (e.g.; lufertility and miscariage), bye disorders (e.g.; glomerulonephritis), conference), reproductive disorders (e.g.; lufertility and miscariage), bye disorders (e.g.; glaucoma and retinal neuropathy). The patients needing restorative therapy the ILI7rip may also be used as antigens in the protent of similar nucleic acids in samples and identify patients needing restorative therapy. The proteins and antigens in the proteins and antigens may also the proteins and activity. The antigens in the production of antibodies against the proteins and in activity. The antigens and are proteins and are equalate contains and are equalated and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and activity.

When the specification but is based on thuman interleukin 17 (11-17) receptor like protein sequence (AMU99904) and has been created according to information given in claim 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 3894; DB 22; Length 738;
Pred. No. 0;
1; Mismatches 4; Indels 14
                                                                                                                                    Miscrdifference 45
/label-: Gly, Pro or Ala
                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page -; 158pp; English.
                                                                                                                                                                                                                                                                                        15-MAR-2001; 2001WO-US08678.
                                                                                                                                                                                                                                                                                                                                        16-MAR-2000; 2000US-189816P.
28-NOV-2000; 2000US-0724460
                                                                                                                                                                                                                                                20-SEP-2001.
                                                  Homo saplens.
Synthetic.
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mutein, Associated
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                                                                                                                                                                                                   WO200168859-A2.
                                                                                                 Key City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jing S;
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240

SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTR 526

467 541

SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTR

WVIQKIHESQFIIVVCSKGMKYFYDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ,480

VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHBSQHGGLDQDCEARPALDGSAALQPL 660

601

661 647 721

LHTVKAGSPSDNPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 720

LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE

PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 752 

AAU09952 standard; Protein; 738 AA.

RESULT 8

8

QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600

LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360

FRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300

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anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzhelmer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leasmic; anti-infertility; ophthalmological; hepatitis; anorexia, cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                Human Interleukin 17 (hIL-17) receptor like protein substitution #2.
                                                                                     Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                         /label- Phe, Leu, Val, Ile; Ala, Tyr
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                 14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                         Misc-difference 227
                                                                                                                                                                                                                                                                                                                                                                                WO200168859-A2
                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                    mutein.
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Gaps

4; Indels 14;

97.0%;

Best Local Similarity 97.5 Matches 733; Conservative

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Query Match

ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120

1 MAPWIQLCSVETVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANBGVGP 60 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRAWGVDTCGWR------GVXP 46

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anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-lathemer's; anti-parkinsonlan; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
                                                                                                                   227. XRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDXIIELVDDTNTTRKVMHYA 286
                                                                                                                                                                                                     361 - LPRERLRPRPKVFLCYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420
                                                                                                                                                                                                                                    VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQOENIYSHLDEESSESSTYTAA 360
                                                                                                                                                                                                                                                                                                                  WVIQKIHESQFIIVVCSKGMRYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480
                                                                                                                                                                                                                                                                                                                                                                                                                                SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Interleukin 17 (hIL-17) receptor like protein substitution #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin 17; hIL-17 receptor like protein; immunomodutatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721 PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        707_PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 738
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28-NOV-2000; 2000US-0724460.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anti-iastimer's, renal, anti-parkinsonian, anti-convulsant, anti-iastimatic, dermatological, osteopathic, vascular, cytostatic, anti-iastimatic, dermatological, osteopathic, vascular, cytostatic, anti-iastimatic, dermatological activities. The IL-17 receptor like moteled acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL)71p) expression. These include, for example-immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. inflammation, diabetes and cransplant rejection), infections (e.g. inflammation, diabetes and cransplant rejection), infections (e.g. inflammation, diabetes and cyting disorders (e.g. alzeinemer's disease, parkinson's disease and epilepsy), uniquidisorders (e.g. alzeinemer's disease, parkinson's disease and epilepsy), clung disorders (e.g. stroke and atherossierosis, and hypercalcaemis), vascular disorders (e.g. stroke and atherossierosis, cancers (e.g. infertility and breast cancers), respectorises and retinal neuropathy). The productive disorders (e.g. infertility and presence of constants and its complements may also used as disquostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 3894; DB 22; Length 738;
Pred. No. 0;
1; Mismatches 4; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page -; 158pp; English
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                                                                                                       ##16-MAR-2000; 2000US-189816P.
##28-NOV-2000; 2000US-0724460.
                                                     15-MAR-2001; 2001WO-US08678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression and activity.

Note: This sequence is not given in the specification but is based on the human interleukin 17 (ILL-17) receptor like protein sequence (AAV09904) and has been created according to information given in claim 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-IL17rlp antibodies and antagonists may also be used to down regulate
                                                                                                                                                                                                                                                                             novel nucleic acids encoding interleukin (IL) 17
                                                                                                     Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        patients needing restorative therapy. The ILI7rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 ASRNSGLINITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTLMSPGALGIE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFRRTGMESQPFLNMKFETDYFVKVVPF 180
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                                                                                                                                      useful for preventing, diagnosing a
                                                                                                                                                                                                                       Claim 23; Page 7, 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.0%;
Best Local Similarity 97.5%;
Matches 733; Conservative 1
                                                                                                                                                                                                                                                                          the invention describes
                                                        WPI; 2001-611392/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     =
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Jing S;
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancectic; anti-alzhemer's; anti-parkinsonian; anti-arshmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma
WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480
                                                                                           SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540
                                                                                                                                                                                                                       407 WYIQKIHESQFIIVYCSKGMKYFVDKKNYKHKGGRGSKGSKGELFLVAVSAIAEKLRQAKQ 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
                                                                                                                         VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL
                                                                                                                                                                                            QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707 PPALPSKILSSGSCKADLGCRSYTDELHAVAP 738
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Misc-difference 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU09955 standard; Protein; 738 AA
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28-NOV-2000; 2000US-0724460.
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The invention describes novel nucleic acids encoding interleukin (IL) 17

Treepfor like polypeptides "useful as vaccines and in gene therapy. These
Communications and interpolyments, anti-schmattic, anti-schmatt, renal,
contributionshain anti-convulsant, anti-schmatto, anti-schmatt, renal,
contributionshain anti-convulsant, anti-schmatto, dermatological,
costeopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
proteins may be used to prevent and treat diseases associated with
coptibulogical activities. The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat diseases associated with
containing the contribution of th pattents needing restorative therapy. The ILL7rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity.

Mote: This sequence is not given in the specification but is based on thuman interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 22. 88<u>8888888888888888888888888888</u>8

Sequence 738 AA;

61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120 FLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNNKFETDYFVKVVPF 180 181 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240 PRFFY LHYKLKHEGPFKRKTCKOEOTTETTSCLLONVSPGDYIIELVDDTNTTRKVMHYA 300 127, FREFILHYRIKHEGPFRRATCKOEQTTETISCLLONVSPGDYIIELVDDINTTRKVMHYA 286 LAPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360 LPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420 4; Indels 14; Gaps MAPWIQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60 Query Match 96.9%; Score 3890; DB 22; Length 738; Best Local Similarity 97.5%; Pred. No. 0; Matches 733; Conservative 1; Mismatches 4; Indels 14 47 121 107 167 341 301 287 361 347 ò 셤 ð a 셤 셤 ð 윱 ò a ö ð 윱 ð

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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; and anti-inframmatory; anti-diabetic; immunosuppressive; anti-nicrobial; hepatic; anabolic; anorectic; anti-alzhelmer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anoresia; cachaxia; neuronal dysfunction; iung disease;
9
                                                               646
                                                                                         LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 720
                                                                                                        bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                Human Interleukin 17 (hIL-17) receptor like protein substitution #7.
                                                  601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL
                                                                                                                                                      707 PPALPSKLLSSGSCRADLGCRSYTDELHAVAP 738
                                                                                                                                           721 PPALPSKLLSSGSCKADLGCRSYTDELHAVAP
                                                                                                                                                                                                                                    AAU09957 standard; Protein; 738 AA.
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                      14-FEB-2002
                                                                                                                                                                                                                                                              AAU09957;
           527
                                                                                          661
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AAU09957
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16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460 15-MAR-2001; 2001WO-US08678 (AMGE-) AMGEN INC. 20-SEP-2001.

/label- Cys, Ala, Ser

WO200168859-A2.

Location/Qualiflers Misc-difference 602

Homo sapiens. Synthetic.

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Jing S;

WPI; 2001-611392/70.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma 

Claim 24; Page -; 158pp; English.

WVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540 541 QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600

5 101 181

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The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, ancectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-ieukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL/7\*Ip) expression. These include, for example immune disorders (e.g. inflammation, diabetes and

Weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzahemer's disease, Parkinson's disease and epilepsy).

Lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eccema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. stoopcrosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and expression and activity.

Note: This sequence is not given in the specification but is based on the human interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 24. patients needing restorative therapy. The ILI7rip may also be used as antigons in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-ILI7rip antibodies and antagonists may also be used to down regulate miscarriage), eye digorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify ASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120 121 FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180 107 FLEGFRVILEELKSBGRQCQQLILKDPRQLNSSFRRTGMESQPFLNMKFETDYFVKVVPF 166 PSIKNESNYHPFFFRTRACDILLQPDNIACKPFWKPRNINISQHGSDMQVSFDHAPHNFG 240 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360 420 1 MAPWIQICSVFFTVNACINGSQLAVAAGSGRAWGVDTCGWR-----GVGP 46 9 hepatitis and septicaemia), PRFFYLHYKLKHEGPFKRKTCKOEQTTETTSCLLONVSPGDY I JELVDDTNTTRKVMHYA MAPWLOLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP LPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE Ouery Match 96.9%; Score 3890; DB 22; Length 738; Best Local Similarity 97.5%; Pred. No. 0; Matches ...733; Conservative 1; Mismatches 4; Indels 14. transplant rejection), infections (e.g. weight disorders (e.g. 738 AA; Sequence 181 241 227 301 361 ~<u>85888888888888888888</u> 셤. 셤 윱 g ö ð ö 요. à ö å

526 WVIQKIHESQFIIVVCSKCMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480 540 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660 587 VLNDVMCKPGPESDFXLKVEAPVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 646 661 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE 720 466 541 GGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL ·600 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLOEPGQHTR 347 121 601 481 셤 셤 ŏ 윱

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RESULT 12

AAU11355 standard; Protein; 738

AAU11355;

26-MAR-2002 (first entry)

Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; gene therapy; protein therapy; immunological disorder

Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.

Homo sapiens.

/label- Val Misc-difference 25

WO200190358-A2

29-NOV-2001.

23-MAY-2001; 2001WO-US16767

24-MAY-2000; 2000US-206862P

(SCHE ) SCHERING CORP.

Gorman DM;

WPI; 2002-106198/14. N-PSDB; AAS18134.

2 Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -

Claim 1; Page 25; 148pp; English.

The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies applied DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRS8 polypeptide. 

738 AA; Sequence

DB 23; Length 738; Score 3830.5; DB 23; Length Pred. No. 0; 2; Mismatches 11; Indels Query Match 95.5%; Best Local Similarity 96.3%; Matches 725; Conservative 2

1 MAPWIQICSVFFTVNACINGSQLAVAAGGSGRARGADTCGWRMRAAARPRLCVANEGVGP 60

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61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAONITISQYACHDQVAVTLMSPGALGIE 120

is N-glycosylated"

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Claim 10; Fig 18; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruman; Interleukin-17 receptor; IL-17RH4; agonist; antagonist;
PR020026; DRA 154095-2998; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; diabetes mellitus;
allergic disease; asthms; demyelinating disease;
degenerative cartilaginous disorder; transplantation associated disease.
                                                                                                                                                              166 SFIKNESNYHPEFERTRACDILLOPDNIACKPEWKPRALAISOHGSDAQVSEDHAPHNFG 225
                                                                                                                                                                                                                             LPRERLARPREVELCYSSKIGGONHANVVQCFAXFLQDFCGCEVALDLARDFSLCREGGRE 405
                                                                                                                                                                                                                                                                          47 ASRNSGLYNITFKYDNCTTYLNPVGRHVIADAQNITISQYACHDQVAVTILMSPGALGIE 106
                      FLKGPRVILEELKSEGROCOQLILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180
                                                                    PSIKNESNYHPFFFRTRACDLILLQPDNIACKPFWKPRNINISOHGSDMQVSFDHAPHNFG 240
                                                                                                                  241 FREFYLHYKLKHEGPFKRKTCKOEGTTETTSCLLQNYSPGDYIIELVDDTNTTRKVMHYA 300
                                                                                                                               LPRERLRPRPRYFICYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420
                                                                                                                                                                                                                                                          WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480
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19..24
/note= "N-myristoyla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04958 standard; Protein; 728 AA.
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Grimaldi CJ;
Vandlen RL;
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                                                                                                                                                                                                  "Tyrosine kinase phosphorylation site"
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:e= "Tyrosine kinase phosphorylation site"
                                                                                                  'note- "cAMP/GMP-dependent protein kinase
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Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M,
Watanabe CK, Williams PM, Wood WI, Yansura DG;
                                                                                                                                                                                                                                                                  "N-myristoylation site".
                                                                                                                                           "Asn is, N-glycosylated"
               Asn is N-glycosylated
                                          note- "Asn 18 N-glycosylated"
                                                                      "Asn is N-glycosylated"
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                                                                                                                                                                      "Transmembrane domain".
                                                                                                                phosphorylation site?
266.,269
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707...71
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N-PSDB; AAS09517.
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18-FEB-2000;
02-MAR-2000;
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30-DEC-1999;
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The sequence is PRO20026 which is the human Interleukin 17 receptor, II-77RH, encoded by DNA 154095-2998. A composition containing ant/agonists to the PRO polypeptides or individual components containing ant/agonists to the PRO polypeptides or individual components on treating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, independent inflammatory myopathy. Sjogren's syndicone, systemic sclerosis, an indipendent inflammatory myopathy. Sjogren's syndicone, systemic vasculitis, ascrodosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated skin disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, an alternatitis, an allegic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneurogathy. Treating a degenerative cartilaginous disorder comprises manner. Numerous examples of the diseases and disorders are given in the specification. 602 SQPFLNMKFETDYFVKVVPEPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLN 220 ETTSCLLONVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327 567 DEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGAT:627 GPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSG1YDSSVPSSE: 687 688 · LSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL 747 42 RMKAAARPRICVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY 100 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKK 447 NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPG1LD 507 Query Match 92.3%; Score 3703; DB 22; Length 728; Best Local Similarity 96.7%; Pred. No. 0; Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 62 -LSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFI 728 AA; Sequence m 423 508 161 123 268 243 388 148 183 999 543 628 603 ¥88888888888888888 ö 요 셤 셤 å 윱 ö ä ò 셤 à 셤 Š δ δ a ð g õ 셤 ò ö ä 윱

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723 HAVAPL_728
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RESULT 14 AAU10602

AAU10602 standard; Protein; 739 AA. 

AAU10602;

14-FEB-2002 (first entry)

Human interleukin 17 (hiL-1) receptor-like protein version 2.

anti-inflammatory; anti-diabetic; immunosuppressive, anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-lendemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human. Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

Homo sapiens.

WO200168859-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-US08678

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC.

Jing S;

WPI; 2001-611392/70. N-PSDB; AAS16201 Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukaemia, asthma, diabetes, psoriasis and glaucoma

Claim 2; Fig 1; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17

The invention describes novel nucleic acids encoding interleukin (IL) 17

The invention describes useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzehmer's, renal, anti-parkinsonian, anti-convulsant, anti-sathmatic, dermatological, osteopathic, vascular cytostatic, anti-leukaemic, duti-infertility and optoteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These incide, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysinction (e.g. Alzhelmer's disease, Parkinson's disease and epilepsy), cup disorders (e.g. oystic fibrosis, asthma and emphysema), skin disease (e.g. stroke and atherosclerosis, asthma and emphysema), skin disease (e.g. stroke and atherosclerosis, cancers (e.g. quantility and business (e.g. stroke and atherosclerosis, cancers (e.g. infertility and miscariage), eye disorders (e.g. infertility may also be used as miscariage), eye disorders (e.g. infertility may also be used an autigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. This is the amino acid sequence of human continuelle and anterestion and activity. This is the amino acid sequence of human continuelle decoration of interleughed in the production of interleugh of the production of the protein described in the method of interleugh of the program of the protein described in the production of an expression and activity. This is the amino acid sequence of human continued to the program of the production of an expression and activity the production of acid and acceptor interleughed to the program of a production of acid and acceptor inter

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             residues 8-296 of the
         Note: Residues 1-288 of this sequence correspond to residues 8-296 of sequence shown in AAU10601 which is incomplete in the specification.
                                                                                                                                                                                                                                                                                              63. RNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDOVAVTILWSPGALGIEFL 122
                                                                                                                                                                       KGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPS 182
                                                                                                                                                                                                                  542
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                                                                                                                                     PGSQQC-----CLHLDSMGLCVG-----RANWLHSASCS---LVFPQGVGPAS 48
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                                                                 Ouery Match 92.3%; Score 3703; DB 22; Length 739; Best Local Similarity 93.7%; Pred. No. 0; Matches 704; Conservative 5; Mismatches 22; Indels 20;
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the invention.
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The invention relates to an isolated cytokine receptor polypeptide designated Ecytor18. The Ecytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with portasis or tumour growth. The encoding nucleic acids are useful for providing Ecytor18 in vivo by gene therapy techniques. Ecytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Ecytor18 probes and primers:can be used to detect and localize Ecytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Ecytor18 gene resides. The Ecytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a murine Ecytor18 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ilgand
Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; humai pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 111-115; 119pp; English.
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299 EFLKGFRVILEELKSEGROCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVP 179 FPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNF 239 Gaps 1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60 GFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHY DB 23; Length 739; Indels 22; 53; Query Match

84.4%; Score 3387; DB
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Murine cytokine receptor, 2cytor18.

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## ALIGNMENTS

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Dmitted to the EMBL Data Library, September 1999 Reference number: 220336 Accession: 727382		ÄÄÄ	;Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: DMA, Molecule 1910
	. <u>.</u>	₹ & & &	; residues: 1-/18 <chi>; residues: 1-/18 <chi>; cessidenetics: EMBL: U39997; PIDN: AAA81100.1; CES</chi></chi>
Cross-references: EMBL: AL110498; PIDN: CAB54470.1; CESP: Y64G10A.e Experimental source: clone Y64G10A		G & S	Jedne: CASF:201/2/, 163/3; 459/1; 517/3; 555/1; 6; Superfamily: Caenorhabditis elegans hypothetical pr
1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3 elegans hypothetical protein Y64G10A.e	* * * * * * * * * * * * * * * * * * * *		Query Match 3.2%; Score 126.5; DB 2; Best Local Similarity 21.1%; Pred: No. 0.091; Matches 82; Conservative: 64; Mismatches 149;
4.2%; Score 170.5; DB 2; Length 846; larity 21.4%; Pred. No. 3.3e-05; Conservative 82; Mismatches 225; Indels 211; Gaps 37;		Oy D	y 363. RERLAPRP
99 QYACHDOVAVTILMSPGALGIEFLKGFRVILEELKSBGRQCQQLILKDPRQLNSSFKRTG 158		g G	Y 413 LCREGOREWVIOKIHESOFIIVVCSKGMKYFVDKRNYKHKGGG
. 159 MESQPFLANKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLIQPDNLAC-KPFWKPR 217   1   1   1   1   1   1   1   1   1	•	40 ·	Y 473 EKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKY :
118 NLAISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLONV 277  183 KLTRIEKPPATSNQTEESDGKAEKDKKEDTWT 415	-	dy Dp	Y 530 HGLOEPGOHTROGSRRNYFRSKSGRSLYVAICNMHOFIDE
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335 CRKKQOENIYSHLDEESSESSYTAALPRERIRPRVFLCYSSKDGONHMNVQCFAYF 394   :		Qy Dp	y 641 LDODGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDS
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GRGSGKGELFLVAVSAIAEKLRQAKGSSSAALSKFIAVYFDYSCEGDYPGILDLSTKY 512		TO TO	4 e-associated recQ-like helicase - es: Ustilago maydis (corn smut)
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SRKLNYIESDPOWFENTHHRYATRRVSELEAHNIVPL-PPSLEVKVEDEDAFGOMETLP1 703 EPVLEKFDSGLVLNDVMCRFQFESDFCLKVEAAVLGATGFADSQHES 636 : :       : :	· · · · · ·	4444	A;Title: Organization of chromosome ends in Ustilago A;Meference number: 216557; MUID:98198830; PMID:95394 A;Accession: T09081 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
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llago maydis (corn smut).
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A: Residues: 1-757 <snn> A: Residues: 1-757 <snn> A: Cross_references: EMBL: AF000885, NID: 92642221; PID: 92642222</snn></snn>	Cremetas: Source Status Far. Argene: UTASrecq Cremetas: DNA binding	Query Match 2.9%; Score 117; DB 2; Length 757; Best Local Similarity 20.4%; Pred. No. 0.57; Matches ::111;;;;Conservative: 56; Mismatches 187; Indels 190; Gaps 27;	OY 268 ETTSCLLONVSPGDYIELVDDNATRRVMHYALRPVRPRAGPIRAVAITVPL 321	QY 322	QY 363RERLAPREVFLCYSSKDGQNHANVVQCF-AYFLQDFCGCEVALDLWEDF,411 :  :  :  :  :  :  :  :  :  :  :  :  :  :	Qy 412 SLCREGOREWIQKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGS 458	QY 459GKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYEDYSCEGDVPGILDLSTKY 512	OY 513RLADNLPQLCSHLHSRDHGLQEPGQHTRQGSRRYFRS 550  1	QY 551. KSGRSLYVAICHMHQFIDEEDDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPG 610  1	OY :: 611. PESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAALQPLLHTVKAG 667  D	OY 668 SPSDMPRDSGITDSSVPSSE-LSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPA 723	Qy 724 LPSK 727  Db 511 PPSE 514	RESULT 5	hypothetical protein F8D20.70 - Arabidopsis thallana C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 23.Apr.1999 \$sequence_revision~23.Apr.1999 *text_change 24-Nov-1999	RiBevan, M.; Rose, M.; Hempel, S.; Entlan, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes, submitted to the Protein Sequence Database, July 1998 A; Reference number: 215381	A; Accessing: 194001 A; Molecule type: DNA A; Residues: 1-917 <bev> A; Cross-references: EMBL: AL031135 A; Experimental: Source: cultivar Columbia; BAC clone F8D20</bev>	₹	C; Superfamily: Arabidopsis thaliana hypothetical protein FBD20.70  Query Match  2.9%; Score 117; DB 2; Length 917;

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Oy 486 C.; Sykes, Db 897 Oy 539 Db 957	C.D.; Fujli, C.Y.;  Qy 599 GLVLADY-WCRPCPESDFCLKYEARIZATG-PASCHESOHGGLDODGEARPALDGSAR  Db 996 NPHDNEIGFDLAGPENSYEDDNYGSLNVPESVRQEKEHG  Vam. L.; Tallon, L.  Db 1036STPVYCDSDSYSINSINTERLSAEIGGISLSISADSAR  1sthallana.	9 RR PR	40,	Query Match 2.9%; Score 116.5; DB 2; Length 901; Best Local Similarity 19.6%; Pred: No. 0.82; Matches 112; Conservative 76; Mismatches 169; Indels 215; Qy 61 ASRNSGLYNITERYDNCTTYLNPVGKHVIADAQNITISQY-ACHDQVAVTILMSPGA 1	Db 372HTFRQEQKRSFAKKREHPYNWRCDETDDVYWCPNORKVSFKRYTKRTDPYGY QY 170 ETDYFVKVVPF-PSIKNESNYHPFFFRTRACDLLQPDNLACKFFWRFR	QY 329 TLPTVMCRKKQOENIYSHLDEESSESSTITAALPRERLRPPRVFLCYSSKDGONHWNVV
Cibate: 12-Feb-1999 \$sequence_revision 12-Feb-1999 \$text_change 16-Feb-2001 C;Accession::T00867; G84891 R; Retchum, R.A.; Crosby, M.L.; Brandon, R. R;Rounsley; S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R submitted to the EMBL Data Library; March 1998 A; Description: Arabidopsis;thaliana chromosome II BAC F17K2 genomic sequence A;Accession: T00867: A;Accession: T00867: A;Status: translated from GB/EMBL/DDBJ	79540; PID:92979554 , T.P.; Benito, M.I.; Town, Shen, M.; Vanaken, S.E.; Uma, J.A.; @lizberg, S.L.; Fras		Query Match . 2.9%; Score 117; DB 2; Length 2946; Best Local Similarity 18.7%; Pred. No. 4.3; Matches 164; Conservative 105; Mismatches 314; Indels 294; Ga 2 APWICACKSYFETUNACLMGSQLAVAAGGSGRARGADTGGWRMKAAARPRICVANEGVGPA 1                                 393 ATWIXIESPADTINAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	0.00   0.00	564 AEMGPVIEKEPIGPERMARIASRGDVLPCFGIGAGLPWLATUDVRN 261 CKOBOTTETTS	OY 384 HANVOCRAYFLODECGEVALDLAMEDFSLCREGGREWLOGNGEEEL-VAALVSLCGSGKIN 786  QY 384 HANVOCRAYFLODECGCEVALDLAMEDFSLCREGGREWVIGKIHESGFIIVVCSKGMK 441  DD 787 HYLKVQLERTLLLDLKIWSLCNYGLGKKLLSSLQDMYFTEATAMRDAEAI 836  QY 442YFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLROAKGSSSAA- 485  DD 837 QLLLDGCRRCYMISEKOSETTFPLGATRAMGHALDELLVIELLAMGAASPSLAAD 896

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OY 484 AALSKEIAVYEDYSCEGDVPGILDLSTRYRLADNLPQLCSHLHSRDHGLQ.533  OY 484 AALSKEIAVYEDYSCEGDVPGILDLSTRYRLADNLPQLCSHLHSRDHGLQ.533  I	OY: 534 EPGQHT	OY 613 SDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDM 672  Db 774YGEQPYMNASNQDDINAVEQDTRLPPPMCPTALHQLMASGWVRDRNLR 822  OY 673 PRDSGIYDSSVPSSELSLPLABGLSTDOT 701  1	RESULT 9  RESULT 9  RESULT 9  S.37627  protein-tyrosine kinase (EC 2.7.1.112), receptor:type - human  C;5pectes: Homo sapiens (man)  C;Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 04-Feb-2000 -  C;Accession: S37627  R;Boehme, B;:Weothme, D;;Wolf, G;; Luzius, H;; Grzeschik, K.H.; Strebhardt, K.; Ru  R;Boehme, B; 2857-2862, 1993  A;Title: PCR mediated detection of a new human receptor-tyrosine;kinase, HEK 2.  A;Reference number: S37627; MOID:93390963; PMID:8397371  A;Accession: S37627	A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Rosidues: 1-998 <bel:x75208; <kin="" a;cross-references:="" atp;="" c;reywords:="" c;superfamily:="" domain:="" embl:x75208;="" eph;="" f;631-699="" fibronectin="" homology="" iii="" kinase="" kinase,="" nid:9406867;="" phosphotransferaes;="" pid:9406868="" pidn:caa53021.1;="" protein="" protein-tyrosine.="" protein;="" receptor="" repeat="" transmembrane="" type="" tyrosine-specific=""> F;639-64/TRegion: protein kinase ATP-binding motif F:922-988/Domain: SAM homology <sam></sam></bel:x75208;>		127 VILBELKSBGRQCQQLILKDPKQLMSSFKR	SPRAGPIRAVAITVPLIVUISARATLFTVMCRKRQGENIYS
613. WEIRIGENVGLIGENGAGKSTTISHISELIOPTSGDVLIKGGSIHKOSKAIRSILGVVPO 672	673 EIAVYHDIAREHLAFFGKIVGLKGEELKHR-MESTLQIV	JULT 8  Specials kinase - mouse (fragment) Specials kinase - mouse (fragment) Specials kina musculuse mouse) Specials kinase musculuse mouse) Specials kinase musculuse Cocassion: [14907] Specials (1990) Specials kinase sapressed in the myocardium of the deve	Generace, unmober: 149071; MUID:95200798; PMID:7893599 (Cepsalon: T49071  Status: preliminary; translated from GB/EMBL/DDBJ  Solecule: type: mRNA  Solecule: mRNA  Sol	<pre>uery Match 2.9%; Score 115.5; DB 2; Length 93%; datches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45; g SVFFTVNACL.NGSQLAVAAGGSGRARGADTCGWRKKAAARPRLC 52  :  :   :   :      :                    </pre>	53 'VANEGVGPASRNSGLINITERYDNCTTYLNPVGKHVIADAQ 93	205 PDNIACKPEWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGFF-KRKTCKQ 263  1	369 RPRVFLCYSSKDGQNHHNVVQCFAYFLQDFC-GCEVALDLWEDFSLCREGGREWVIGKIH 427      :

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149239 Vegicle transport protein - mouse C;Species: Mus musculus (house mouse) C;Date: 02:Jul-1996 \*sequence\_revision 02-Jul-1996 \*text\_change 05-Nov-1999

QY 405 LDLMEDPSLCREGOREMVIQKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELF 464		
ONLINGEORINGER  A 65. IVAVCATARREDOAR OCCAAT CERTANDERNOCHEODER CT. T. T. C		
662 -VALKTLKVGYTERORADFLSEASINGOFDHPNITE FGVUTERPOWT		
Db. 710; LTEFMENC-ALDSFLRLNDGQFTVIQLVGMLRGIAAGMKYLSEMNYVHRDLAAR 762.		
QY 555 SLYVALCNAGQFIDEEPDWPERQFYPFHPP		
UY 598 SGLVLUNVACREGEESDRCLKVEAAVLGATGEADSQUESQUGGLDQDGEARRA 650 DD 11: 1: 1  1 :: 1  1 :: 1  1   1 :: 1  1   1		
QY 651 LDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGL 696		
Db 861 MDCPTALRQLMLDCWVRDRNLRPKFSQIVNTLDKLIRNAASLKVIASAQSGMSQPLLDRT 920	-	
OY 697 STDQTETSSLTESVSSSGLGEBEPPALPSKLLSSGSCKADLGCRSTTDEL 747		
Db 921 VPDYTTFTTVGDWLDAIR-MGRYKESFVSAGFASFDLVAQWTAEDL 965		
RESULT 10		
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: How sapiens (man)		
.UCT-1999 #Sequence_revision 15-Oct-1999 #tex		
A.P. Polista, A.; Klehn, M.; Mowes, H.W.; Gassenhuber, J.; Wiemann, S. Submitted to the Protein Sequence Database, September 1999	٠.	
A;Cross_references: EMBL:AL117401 A;Experimental source: adult testis; clone DKF2p434P211 A;Note: the CDNA.sequence contains a .1 frameshift near codon 488 C;Genetics:		
A; Note: DRF2p434P211.1		
Query Match 2.7%; Score 110; DB 2; Length 535; Best Local Similarity 23.5%; Pred. No. 1.3; Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;	17;	
N. L.P	•	
OY 521 LCSHLHSRDHGLOEPGQHTRQGSRRNYFRSKSGRSLIVAICNMHQFIDEEPDWFEKQF 578		
DD 163 AVSSGHTQCEKAADIAPGQTLTLRNDSSTSEASRPSTHKFPLLPRRRG 210	,	_
OY 579 VPFH-PPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAA 622		
Db 211 EPLALPPPLELGYRVTVEDLDREKEAAFQRINSALQVEDRAISDCRPSRPSHTLSSL 267		
OY 623. VLGATG-PADSQHESOHGGLDQDGBARPALDGSAALQPLLHTVKAGSPSDMPRD 675		
LAEGISTDOTETSSLTESVSSSGLGEEEPPALPSKLLSSG 73		
322 PGPLESSSDPLPATSSDSQDSAQVTSLIPAPFPAASMDAG		

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R;Tellam, J.T.; McIntosh, S.; James, D.E.
J. Biol. Chém. 270, 5857-5863, 1995
A;Tille: Molecular identification of two novel Munc-18 isoforms expressed in non-neur
A;Reference number: 149238; MUID:95197608; PMID:7890715
A;Accession: 149239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Mori, M.; Nishikawa, T.; Higuchi, K.;.Nishimura, M. submitted to the EMBL Data Library, November 1998 A:Description: Deletion in the beige gene of the beige rat due to recombination betwee A:Reference number: 217837 A:Accession: T13960
                                                                                                                                                                                                                                                          Query Match 2.7%; Score 110; DB 2; Length 592;
Best Local Similarity 18.5%; Pred. No. 1.5;
Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                      321 LVVISAFATLFTVMCRKRQQ-------BNIYSHLDEESSESSTYTAALPRERLRPRPR 371
                                                                                                                                                                      A;Cross-references: EMBL:U19521; NID:g642027; PIDN:AAA69913.1; PID:g642028
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 SVDCFLRDFGSKSEKKYKAAYIYFTDFCPDSLFNKIKASCSKSIRRCKEINISFIPQESQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403 -VALDLWEDFSLC-----REGOREWIQKIHESQFIIVVC-----SKGMKY------ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 SKLAQLVEKKLEDYYKIDEKGLIKGKTQSQLLIIDRGFDPVSTVLHEL------ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313.STK.....RATEGRISLSALTQLMKKNPHFRKQISKOVV-----HL.348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488 KFIAVYFD-----YSCEG-DVPGIL----DLSTKYR-----LMDNLPQLCSHLH 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 TFQAMAYDLLPIENDTYKYYTDGKEKEAVLEEDDDLWYRVRHRHIAVYLEEIPKLMKEIS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527 SRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNNHQFIDEEPDWFEKQFVPFHPPPL 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------DSGLVLNDVMCKPGPESDFCLKVE 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 ----FVDKK---NYK--HKGGGRGSGKGELFLV----AVSAIAEKLRQAKQSSSAALS 487
                                                                                                                                                                                                                                                                                                                                                                                                 34 IMLIDEFTTKLISSCCRWTDLIEBGITVIENITRNREPVROMKALYF-----SPTPK 86
                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: T42730 . q å 윱 ö 8 a ö ö ò ò Ribleck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cedl Biol. 142, 499-569, 1998
Affitle: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A; Reference number: Z2249; MUID:99345363; PMID:9679147 38; C:Species: Mus musculus (house mouse) C:Date: 11.7an-2000 #sequence\_revision 11.7an-2000 #text\_change 21-Jul-2000 C:Accession: T47730 1125 -----SIGLENILCELRDHISQSKVAETELAKPLFDALLRVALGHHSADLDPGDT 1174 508 --LSTK--------YRLANDNLPQLCSH---LHSRDHGLQEPGQHTRQG 542 592 VLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATG-----PADSQHESQHGGLDQDGE 646 744 ELVHHCQQLSI-----TSAQTHMSSQLKQYLQYLQGYLQIYLKTLPILLKSRVIRDLFL 795 230 VSFDHAPHNFGFRFFYLHYKLKKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDD 289 853 V-----FYASLRD 880 290 TNITRVWHYALKPVHSPWAGPIRAVALTVPLVVLSAFATLFTVMCRKKQOENIYSHLDE 349 881 DPKKRTVHQ------DAHINTINLELCVAF-----LCVSKEADSDRESAN- 920 458 SGKGELF----LVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD---- 507 696 YONFIFOE--DRIHNTQIASHICHLIQKGNVIVOM-----KLYNYIFNPVLQRGV 743 137 --- RQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFET-DXFVKVVP-----FP 181 350 ESSESSTY--TAALPRERLRPRPKVFLCYSSKDGONHMNVV----QCFAYFLQDFCGCEV 403 404 ALDLWEDFSLCREGOREWV -- IQKIHESQFI----IVVCSKGMKYFVDKKNYRHKGGGRG 457 543 SRRNYFRSKSGRSLYVAICNMHQFIDEEP-----DWFEKQFVPFHPPPLRYREP 591 Gaps A.Gene: baigers: 17 200 Agrica out Matchesse 7 200 Matches Similarity: 19.4%; Pred: No. 31; Score Logers Similarity: 19.4%; Pred: No. 31; Score Logers Similarity: 19.4%; Pred: No. 31; Score Logers Similarity: 19.4%; Matches 2017; Indels 235; Score Matches 2017; Indels 235; 1232 ELPEAEGFSGSIVPNNLLESLTHG 1255 647 ARPALDG-SAALOP--LLHTVKAG 667 Bassoon protein - mouse 921 RESULT 13 염 셤 ୍ଘ ୃଷ୍ଟ ପି ୍ଷ 요 ŏ 셤 <sub>)</sub> 옵 셤 음 ò .. 음 ζò · & 셤 ŏ ି ο̈ ŝ . 쉽 ~ &

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A: Description: may be involved in cytomatrix organization at the site of neurotransmi A;Note: component of the presynaptic cytoskeleton C;Reywords: colled coil; zinc finger
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R; Barbosa, M.D.F.S.; Tchernev, 'V.T.; Kingsmore, S.F.
submitted to the EMBL Data Library, September 1996
A; Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) gene.
A; Reference number: 220903
                                              A;Residues: 1-3942 CDIE>
A;Cross-references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810
A;Experimental source: strain 129 SVJ
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AAC53011.1
A; Experimental source: strain C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3590 TDWFDK---PRDARSDRFRHHGGHTVSSSQKRGPARHSYHDYDEPPEEGLWPHD---EGG 3643
                                                                                                                                                                                                                  A;Map position: 9F1
A;Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lysosomal trafficking regulator, long splice form - mouse N.Alternate names: beige protein homolog C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Date: 22-0ct-1999 #sequence_revision 22-0ct-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | | | | : : | | : : : | | : | | : | | 3535 DICPOPECS-----SHSMPDVQEHVKDGPRAHAYKREEGYMLDDSHCVVSDSEAYHLGQEE 3589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3644 PGRH------TSAKEHRHHSDHGRHSGRHAGEEPGRRAAKPHARDMGRHEARPH 3691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAIC -----NMHQFIDEE 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665 KAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPAL 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611 PESDFCLKVEAAVLGATGPADSQHESQHG-----GLDQDG-------EARP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650 -----ALDGSAALQPLLHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   f Match 2.7%; Score 107.5; DB 2; Length 3942; Local Similarity 19.1%; Pred. No. 39; national SB; Conservative 29; Mismatches 99; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.7%; Score 107; DB 2; Length 3788; Best Local Similarity 19.5%; Pred. No. 40; Matches 156; Conservative 104; Mismatches 288; Indels 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-3788 <BAR>
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      651 GETLOGTLCGAGPTSGLPSPSYRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: alternative splicing
                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11:
3809 PSQ 3811
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                                                                                                                                                                                                                                                                                            A; Note: bassoon
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: Lys
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references: GB:AE005172; NID:g8778345; PIDN:AAF79353.1; GSPDB:GN00141

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	A. Accession: D86477 A. Status: preliminary
· .	A. T. Tutle: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A. Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A. Reference number: A86141; MUID: 21016719; PMID: 11130712
	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
	Hunter, J. H.; L1,
.•	Riffeologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Nature 408.
	C:Species: Arabidopsis thallana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accession: D86477
	RESULT 15 D8640 PF1504.27 [imported] Arabidopsis thaliana
	1260
Search completed: May 6,	ON 719 PRODALDSTITECTOREN 738
Db 617 IFCSL 621	663 TVKAGSPSDMPRDSGIYDSSVPSSELSLPLAMEGLSTDQTETSSLTMESVSSSGLGE-:   :   :   : :     : : :     : :   : :     :   : :     :     :
Qy 559 ALCIN 563	DD 1149 LAKPLFDALLRVALGNHSADLGPGDAVTEKSHPSEEELLSQPGDFSERAEDSQCCSLKLL 1208
AY CTANAGE OF THE PROPERTY OF	609 - PODESDECTRUERAN
554	QY 553 MHQFIDEEPDWFEKQFVPFHPPPLRKFDSGLVLMDVMCK: 608
OY 442 YFVDKKNYKHKGGGRC	1049
517	QY 512 YRLMONLPQLCSHLHSRDHGLQEPGQHTRQGSRRNXFRSKSGRSLYVAICN 562
382	1012 GEMSRNENGELIRISYPELTLKODYSSATAPDLGFL
OY 327 FATLFTVMCRKKOOEN : :: : ::  Dh 458 PNSKDETICKVCKRR	DD 901 DLWSMCKMIYMLMSVEQKQFHRLGGFQVCHE-LIFMIIQKLFRSHTEDOGRR 1011 Ov 460 KGELFLVAVSAIAFRIROAKOSSSAALSKFFTAVFFFYSCFGNVGTI
DD 417 GFSYICSNKGCQDE	907
OY 267 TETTSCLLONVSPGDY	Db 917 ESANESEDTSGYDSPPSEPLSHALPCLSLEDVVLPSPECLHHAA 960
Db 365 HQFYHCKKCNYSLHEN	QY 350 ESSESSTYTAALPRERLRPRPKVFICTSSKDGONHMNVVQCFAXFLQDFCGCEVAL 405
QY 211 KPFWKPRNLNISQHG	D 681 DPKKRKTHQDVHINTINLELCVAFLCVSKEADSBR 916
154	853 VFYASLREP
Db' 275 DIKYGQYSCHLQDCFY	QY 230 VSPDHAPHNEGEREFYLHYKLKHEGPEKKTCKQEQTTETTSCLLQNVSPGDYIELYDD 289
	796 SCNGVNHIIELAYLADGIRSHSLKAFETLIVSLGBOOKDAAVLDVDGLDIQQELPSLS
Best Local Similarity :- Matches 94: Conservat	18. SIKNESNYHPF-FFRRACDILLOPDILACKPEWKPRILLISCHGSDMO
A; Map; position: 1	Qy :: 137PP 181  Oy :: 137PP 181  I
A; Cross-references: GB: AEC C; Genetics:	DELIG 696 YOSEVEQEDELHNIQIANHICHLIQKGNVVVQWKLYNYIENPVLQRGV 743
A: Molecule type: DNA A: Residues: 1-638 <sto></sto>	OY " 680 YIMPVORHVIADAQNITISOYACH - DOVAVTILWSPCALGIEFLKGFRVILEELKSEG - 136
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GFSYIC--SNKGCQDFVLDV-----RCISVLEYFIHRSHEH-------PIFISTS 457
Match 2.7%; Score 106.5; DB 2; Length 638; ocal Similarity *19.4%; Pred: No. 3.1; s. 94; Conservative 63; Mismatches 175; Indels 153; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TETTSCLLONVSPGDYIJELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNSKDEILCKVCKKRCLGAHLQCTLCEFTMCYSCAIIPDEIHYRFDKHPLTLSCGESAD-516
                                                                                                                                      NITISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSS 153
                                                                                                                                                                           5 DIKYGOYSCHLODCHYVVHS-----KCATHENVWDGKELEWEIESDETEDISP 322
                                                                                                                                                                                                                                                                     4 FKRIGMESOPFLNMKFETDYFVKVVPFP --- SIKNESNYHPFFFRTRACDLLLOPDNLAC 210
                                                                                                                                                                                                                                                                                                                     1 RPFWRPRNLNISQHG---SDMQVSFDHAPHNFGFRFFYLHYKLKHEGP--FKRKTCKQEQT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FATLFTVMCRKKQQENIYSHLDEESSE-SSTYTAA-LPRE---RLRPRPKVFLCYSSKDG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NTYWCEV------CEROLDPREWFYTCNK-----CCITIH------LHCIFGSS 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGD 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SIFRDYYGKVQ 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRN--YFRSKSGRSLY-V 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VFM-----KPG------KPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AICNM 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ::
7 IFCSL 621
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completed: May 6, 2003, 13:45:47 :: 60 secs

GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd. 

ON protein - protein search, using sw model

Scoring table: BLOSUM62 Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

### SUMMARIES

:		·- 🐠			SUMMARIES		
Result	,	Query					
2	Score	Match	Length	g :	er G	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Description
-	310	7.7	998	-	I17R_HUMAN		Q96f46 homo sapten
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m ·	135.5	۳. ۳.	203	-	I17S_HUMAN	-:	
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<b>.</b>	115	6.6	866		EPB3_HUMAN		P54753 homo saplen
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7	110	2.7	592	-	STB3_MOUSE		_
<b>60</b> 1	104	9	1462	-	PTP6_DROME		P16620 drosophila
σ;	103.5	7.6	663		RGP2_HUMAN		6 homo
10	102	ω, ω,	829	-	ABR_HUMAN		9 ношо
=	101	2.5	1275	-	GNRP_HUMAN		2 homo
17	100.5	.5	974	-	RHG6_HUMAN		043182 homo sapien
13	99.2	2.5		-	Z151_MOUSE		I mus m
17	56	2.5	783	Н	ZFY2_MOUSE	,	2 mus
15	66	2	970	-	- 1	٠.	P53550 saccharomyc
91	98.5	N.	. 993	-	EPB3_MOUSE		P54754 mus musculu
17	98.5	.5	1050	-	EX5B_CHLPN		Q9z7g7 chlamydia p
18	86	7	820	-	CTNB_TRIGR	÷	P35223 tripneustes
15	37.5	7.	1845	<b></b>	2236_HUMAN	٠.٠	6 homosa
50	97	7	984	-	EPB1_CHICK		Q07494 gallus gall
21	97	7	86	<b>-</b>	EPB1_RAT		•
22	96.5	7	746	<del></del>	ABLUMLVAB		P00521 abelson mur
23	96.5	7.7	905	<b></b> 1	EPBB_XENLA		6
24	96	7.	424	<del></del> .	MK09_HUMAN		-
93	9	7.7	999	н.	HT31_ARATH	7	Q04996 arabidopsis
76	96	7.	1114	<b>м</b> ,	E2K3_MOUSE		_
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. 78		7.7	933	-	PRGR_HUMAN		1 homo sa
53	95	7	1036	Н,	AXO1_CHICK		io
20	94.5	7.7	351	<b>-</b>	- 1		P20271 caenorhabd1
31	5.5	7.7	770	<b>-</b>	GIT1_RAT		Q9z272 rattus norv
35	94.5	7	841		IE63_MCMVS		Q69154 murine cyto
33	94.5	7.	1011	-	M3K6_HUMAN		095382 homo sapien
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•			drosophila			coturnix co		rattus		mus mu	ч	gallus gall	•
	P54762	P91620	P91621	P49792	004982	P34908	061548	005140	P01855	062421	P98154	073775	•
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	EPB1_HUMAN	SIF2_DROME	SIF1_DROME	RBP2_HUMAN	RMIL_CHICK	RMIL_COLUA	A180_MOUSE	A180_RAT	"EPC_RAT"	SH33_MOUSE	IDD_MOUSE	FBL1_CHICK	
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	<b>.</b> 94	94	94	94	93.5	93.5	93.5	93.5	93	92.5	92.5	92.5	
	34	35	36	37	38	33	.04	41	42	43	44	<b>\$</b>	

## ALIGNMENTS

RESULT 1

114542499888888888888888888888888888888888	TR. HUMAN  117R. HUMAN  117R. HUMAN  117R. HUMAN  117R. HUMAN  117. 2002 (Rel. 41, Last so  15-JUN-2002 (Rel. 41, Last so  15-JUN-2002 (Rel. 41, Last so  15-JUN-2002 (Rel. 41, Last so  11.17R.  HOMO Saplens (Human).  HOMO Saplens (Human).  HUMAN HERACAS; Chordata; Primates; Mammalla; Butheria; Primates; MCBL_TAXID=966;  101  SEQUENCE FROM N.A.  TISSUE-T-cell; Primates; MCBL_TAXID=966;  YandenBos T., Zappone J., Pal MODIECHE, PROFICE FROM N.A.  TISSUE-HEALUSE SPOOR (1997).  21 SCOUENCE FROM N.A.  TISSUE-Uterus; Strausberg R.; Derry J.  22 SEQUENCE FROM N.A.  TISSUE-Uterus; Strausberg R.; Submitted (JUL-2001) to the E SUDMALITOR. Receptor for IL SUBGELIGAR (JUL-2001) to the E SUDMALITOR. Receptor for IL SUBGELIGAR (JUL-2001) to the E SUDMALITOR. RECEPTOR TISSUE SPECIFICITY: Hidell - TISSUE	LIANDORALN 342 DOMAIN 810 CARBOHYD 49 CARBOHYD 54 CARBOHYD 206
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                                                                                                                                                                                                                                                                                                                                                                                      -i--FUNCTION: Receptor for IL17. Binds its ligand with low affinity, suggesting that additional components are involved in IL17-induced signaling (By similarity).

-i- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 YI----NLSVSSTQHGELVPVLHVEWTLQTDASILYLBGAELSVLQLNTNERLCVKFQF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: |: |: | : | 132 LSMLQHHRKRWRFSF-----SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 HVIADAQNITISQYACHDQVAVT-ILWS-PGALGIEFLKGFRVILEELKSEGRQCQQ----141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 --LILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRAC 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNVSPGDYIIELVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 GWRM-----KAAARPRL-----CVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 GWLLLLLINVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNI 76
                                                                                                                                                                                                                                 Tao Z., Fanalow W.C., Seldin M.F., Rousseau A.M., Painter S.L., Comeau M.R., Cohen J.I., Spriggs M.K.; Herpesvirus Salmiri encodes a new cytokine, IL-17, which binds to
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalta; Eutherla; Rodentia; Sciurognathl; Muridae; Mus
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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llarity 22.5%; Pred. No. 1.1e-15;
Conservative 128; Mismatches 319; Indels 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAC) MOLITALY, Transmembrane; Signal; Glycoprotein.
SIGNAL 1 31 POTENTIAL.
CHAIN 32 864 INTERLEUKIN-17 RECEPTOR.
DOMAIN 32 322 EXTRACELULAR (POTENTIAL).
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                                                                                                                                                                        TISSUE-Thymic lymphoma;
MEDLINE-96111968; PubMed-8777726;
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                                                                                                                                                                                                                                                                                                                             novel cytokine receptor.";
Immunity 3:811-821(1995).
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343
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is SWISS-PROT entry is copyright. It is produced through a collaboration tween the SWISS Institute of Bioinformatics and the EMBL outstation e European Bioinformatics Institute. There are no restrictions on its e by non-profit institutions as long as its content is in no way diffied and this statement is not removed. Usage by and for commercial
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N-KINKED (GLCNAC...) (POTENTIAL).
N-KINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                         SUBCELLUIAR LOCATION: Type I membrane protein (1soform 1);
Secreted (1soform 2).
ALTERNATIVE PRODUCTS: 2 1soforms; 1 (shown here), and 2; are
produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in several endocrine tissues, mostly
in fetal and adult liver, kidney, pancreas, testis, colon, brain
and small intestine; not detected in peripheral blood leukocytes,
lymphold organs, and most cell lines.
                                                                  e.J., Ho W.H., Maruoka:M., Corpuz R.T., Baldwin D.T., Foster J.S., e.J., Ho W.H., Maruoka:M., Corpuz R.T., Wood W.I., Gurney A.L.; L-17R, a. novel. proinfiammatory ligand for the IL-17 receptor homolog-17Rhl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 NLNISQHGSDMQVSF-----DHAPHNFGFRFFYLHYKLKHEGPFKRKTC------ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 -----KQEQTTE----TISCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 313
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                                                                                                                                                                                                                                                Receptor for the proinflammatory cytokines ILI78 ay play a role in controlling the growth and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BL; AF208111; AAF86052.1; -
BL; AF212365; AF78776.1; -
BL; AF212309; AAK37428.1; -
BL; BC000980; AAK30480.1; -
new; HGNC:18015; IL17BR.
new; HGNC:18015; IL17BR.
ceptor; Transmembrane; Signal; Glycoprotein; Alternative
GRAL
AGNAL
18 502 INTERLEUKIN-17B RECEPTOR.
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HISSING (IN REF. 2).
L -> F (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERLEUKIN-17B RECEPTOR.
EXTRACELULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
mitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDB87586FAAE49CC CRC64;
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MISSING (IN ISOFORM 2).
L -> I (IN REF. 1).
                                                                                                                                                                                                                                                                              IL17E. May play a role in controlling the differenciation of hematopoletic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tities requires a license agreement (send an email to license@isb.sib.ch)
                                                                                                                                                                                                                 Biol. Chem. 276:1660-1664(2001)
FUNCTION: Receptor for the pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BL; AF208110; AAF86051.1; -. BL; AF208111; AAF86052.1; -.
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55884 MW;
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502 AA;
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es 76; Conserv
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Y SO.	JIT 4	-	AC.
22555	(Rel. (Rel. (Rel.		OSS
38888	Appointerioal 81.0 KDM protein K3bD1.2, in chromosome II precursor. F56D1.2. Caenorhabditis.elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.		20 0 K R 9 0 5
8 8 8 8 <del>8</del>	[1] SEQUENCE FROM N.A. STRAIN-BILSTOL N2; Chissoe S., Wilson R.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases		7 7 7 8 8 X
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SEFFFS	EMBL; 039997; AAA81100.1;		88888888
Q W X	Query Match 3.2%; Score 126.5; DB 1; Length 718; Best Local Similarity 21.1%; Pred. No. 0.064; Matches 82; Conservative 64; Mismatches, 149; Indels 94; Gaps 19;		ម ខ្លួន ខ្លួន ខ្លួន ខ្លួន ខ
ç q	363 RERLRPRPKVFLCYSSKDGQNHANVVQCFAYFLQDFCGCEVALDLWEDFS 412   ::      :      :  :      :  :      :  :		DR DR DR
95 65	413 LCREGOREMVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIA 472   1	<b>8</b> W	
2 6	473 BKLRQARQSSAALSKFIAVYEDYSCEGDVPGILDLSTKYRLHONLPQLCSHLHSRD 529 :		8 8 8 8
Oy Op	530 HGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNHHQFIDEEPDWFEKQFVP 580	· .	******

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                                                    620 LH---LKRQSPVIVPIQT-------EED---RIAASIKINLVPPQALVDSD----657
                                                                                                                                641 IDQDGEARPALDGSAALQPLLHTVKAGSPSDM--PRDSGIYDSSVPSSELSLPLMEGLST 698
581 FHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGG 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
--- SUBCELLUIAR LOCATION: Type I membrane protein.
--- TISSUE SPECIFICITY: UBIGUITOUS.
--- SIMILARITY: CONTAINS 1 SAM DOMAIN.
--- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
--- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boehme B., Holtrich U., Wolf G., Luzius H., Grzeschik K.-H.,
Strebhardt K., Ruebsamen-Waigmann H.;
"PCR mediated detection of a new human receptor-tyrosine-kinase, HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-W.T-2001 (Rel. 40, Last annotation update)
Ephrin type-B receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein mins, receptor HER-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1. FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO EPHRIN-B1 AND -B2.
-1. CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and the
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the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
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entities requires a license agreement (See )
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                                                                                                                                                                                                                                                                        :: 699 DOTETSSLTESVSSSGLGEREPPALPSK 727
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IPR003962; FN_III_repeat.
IPR001660; SAM.
IPR001245; Tyr_pkinse.
IPR001426; YKASe_receptorV.
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MEDLINE-93390963; PubMed-8397371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase receptor HEK-2
EPHB3 OR ETK2 OR HEK2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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QY   514LADNLPQLCSHLABRDHGLQEPGQHT	651 LDGSALQPLLHTVKAGSPSDMPRDSGIYDS- 651 LDGSALQPLLHTVKAGSPSDMPRDSGIYDS- 1   1   1   1   1   1   1   1   1   1   1	Q9JIP3; Q9JIP2; 15-70N-2002 (Rel. 41, Created) 15-70N-2002 (Rel. 41, Last sequence u 15-70N-2002 (Rel. 41, Last annotation Interleakin-17B receptor precursor (I homolog 1) (II-17Rh1) (IL17Rh1) (IL-1 IL17BR OR EVI27. Mus musculus (House). Eukaryota; Metazoa; Chordata; Cranlat Mammalla; Eutheria; Rodentia; Sclurog NCBL_TaxID=10090;	RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  RX HEDLINE-2027323; PubMed=10815801;  A Tian E., Sawyer J.R., Largaespada D.A., Jenkins RA Shaughnessy J.D. Jr.;  RT "EV127 encodes a novel membrane protein with hon receptor.";  T neceptor.";  RL Oncogene 19:2098-2109(2000).  C FUNCTION: Receptor for the proinflammatory of ILIJE. May play a role in controlling the grant differenciation of hematopoletic cells.  C -1-SUBCELLULAR LOCATION: Type I membrane protein	CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown by produced by alternative splitcing.  CC -1- TISSUE SPECIFICITY: Liver and testis: Expressive splitcing.  Aldney and lung. Expressed in selected T-cel lines.  CC -1- MISCELLANDOWS: EVIZ7 is a common site of ret common muthon myeloid leukemias, localized near proviral integrations result in increased escent common selected.  CC the cell surface.	C This SWISS-PROT entry is copyright. It is produce the Swiss Institute of Bioinformatics controlled the Swiss Institute of Bioinformatics C the Ruropean Bioinformatics Institute. "There are condified and this statement is not removed. Use C modified and this statement is not removed. Use C entities requires a license agreement (See http: CC c rsend an email to licenseelib.sib.ch).  REMBL; AF208108; AAF86049.1;  DR EMBL; AF208109; AAF86050.1;  NGC; MGI:1355292; Ill7br. 1; BR Receptor; Transmembrane; Stynal; Glycoprotein; FT STGNAL 17 BY STHILARITY.  FT CHAIN 2 18 499 INTERLEGININ-17B REC
		i <del>Granda</del>			
**EPhril_rece **ENT: 2.** **SAM: 1.** **SAM: 1.** **PROFEIL_RIN **PROFEIL_RIN ***PROFEIL_RIN **PROFEIL_RIN ***PROFEIL_RIN ***P	SIGNAL   33   POTENTIAL   1998   EPHRIN TYPE-B RECEPOR 3   1998   EPHRIN TYPE-B RECEPOR 3   1998   EPHRIN TYPE-B RECEPOR 3   1998   ETRACELLULAR (FOTENTIAL)   1999   CYTOPLASNIC (POTENTIAL)   1999   CYS-RICH   1999   CYS-RICH   1999   1960   196	E, 758 758 BY SIMII 608 608 PHOSPHOR 614 614 PHOSPHOR 792 792 PHOSPHOR 942 942 PHOSPHOR D 351 351 N-LINKEL E 998 AA, 110286 WW, 57C87 A 2.94; Score 11 SAMILARITY 19.09, Pred, WG, 581 COARD 19.00	GADTOGWRMKAAARPRICVANEGVOPASRNSGLYNITFK	182 SIRRESNYHPFEFRTRACDLIQPDNIACKPEWRRRILNISOHGSDMOVSFDHAPHNEGF 241  1	TYSERGREGAQUOEQLPLIVGSATAGLVFUVAVVIALVCLRKQRH TYTAALPRERLRPRYVELCYSSKDGQNHMNVQCFAYFLQDFC-GCEVA

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Sec. 19 . 19 . 10.

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IPR001619; Sec1-11ke.
   InterPro; IPR001619; Sec
Pfam; PF00995; Sec1; 1.
Protein transport.
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                                                                             Query Match
                                                                                              Local
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                        CTIOPLASHIC (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)

LNHYMKKKKQCTEAGSLADPDITACKKNEKNVEVNETINPL
                                                                                                                   GNRYTILIQRDTTLG -> TRENTEVISGVEPAAKHQALRI
SAPPFLQPPROPEDSYLLPPOPLASLEHDEVKLT (IN
ISOFORM 2).
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                    Similarity 24.14; Pred. No. 0.66; Tonservative 27; Mismatches 7.82; Indels 17; Gaps
                                                                                                                                                                                                                                                                355 STYTAALPRERLRPRPRVFLCYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLC 414
                                                                                                                                                                                                                                                                                   415 REGOREWVIONIHESOFIIVVCSKGMKTFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEK 474
                                                                                                                                                                                                                                                                                                                                           30-MXY-2000 (Rel. 35, Last sequence update)
Syntaxin binding protein 3 (UNC-18 homolog 3) (UNC-18C) (MUNC-18-3),
STXBP3 OR UNC18C.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95197608; PubMed-7890715;
Tellam J.T., McIntosh S., James D.E.;
"Molecular identification of two novel Munc-18 isoforms expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentla, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            defects in
                                                                                                                                                                                                         2.8%; Score 110.5; DW1; Length 499;
    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gengyo-Ando K., Kitayama H., Mukalda M., Ikawa Y.;
"A murine neural-specific homolog corrects cholinergic de
Caenorhabditis elegans unc-18 mutants.";
J. Neurosci. 16:6695-6702(1996).

J. Neurosci. 16:6695-6702(1996).

-- TISSOB SPECIFITY: UBIQUITOUSIX EXPRESSED.

--: SIMILARITY: BELONGS TO THE STXBP/UNC-18/SEC1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                  475. LRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQ 520
                                                                                                                                                                                                                                                                                                                                                                                                             431 F----SSQTHLHKYLVVYL------GGADLKGDYNALSVCPQ 462
                                                                                                                                                                             C66440430E3C31F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 592 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 270:5857-5863(1995)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/c; TISSUE-Brain;
MEDLINE-96421662; PubMed-8824310;
                                                                                                                                                                             55617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U19521; AAA69913.1; -
                                                                          156
197~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:107362; Stxbp3.
                                                                                                                                                                                                            •
                                                                                                                                                             219 4
499/AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-neuronal tissues
                                                                                                                                                                                                          / Match .
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STB3_MOUSE
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                      CARBOHYD VARSPLIC
                                                                                                                                                             VARSPLIC
                                                             CARBOHYD
                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                    87 SVDCFLRDFGSKSEKKYKAAYIYFTDFCPDSLFNKIKASCSKSIRRCKEINISFIPQESQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 -VALDLWEDFSLC-----REGGREWVIQKIHESQFIIVVC----SKGMKY----- 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFIAVYFD-----YSCEG-DVPGIL----DLSTKYR-----LADNLPQLCSHLH 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPL 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STK------HL 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%; Score 110; DB 1; Length 592;
18.5%; Pred: No. 0:92; Vec. 64; Mismatches 157; Indels 188; Gaps
                                                                                                                                                                                                  321 LVVISAFATLFTVMCRKKQQ---------ENIYSHLDEESSESSTYTAALPRERLRPRPR 371
                                                                                                                                                                                                                                                                                                                                  147 VYTLDVPDAFYYCYSPDPSNASRKEVVMEAMAEQ -- IVTVCATLDENPGVRYKSKPLDNA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 ----FVDKK---NYK--HKGGGRGSGKGELFLV----AVSAIAEKLRQAKQSSSAALS 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLAEDCMNKFKLNIEKLCKTEQDLALGTDAEGGRVKDSMLVLLPVLL--NKNHDNCDKIR 406
                                                                                                                                                                                                                                              34 IMLLDEFTTKILSSCCKWTDLLEBGITVIENIYKNREPVROMKALYF-----ISPTPK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
-1- FUNCTION: IT IS POSSIBLE THAT DPTP IS A CELL ADHESION RECEPTOR.
-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 - protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryots, Metazoa, Arthropda, Mandibulata; Pancrustacea; Hexapoda;
Insecta, Pteryota; Neoptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.; *A family of receptor-linked protein tyrosine phosphatases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.40G-1990 (Rel. 15, Created)
01.40G-1990 (Rel. 15, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-tyrosine-phosphates phosphohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 SKLAQLVEKKLEDYYKIDEKGLIKGKTQSQLLIIDRGFDPVSTVLHEL-----
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--- SUBCELLULAR LOCATION: Type I membrane protein.
--- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SEQUENCE 592 AA, 67942 MW, 77874B71DE107871A CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1462 AA:
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                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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NCBL_TaxID-7227;
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us-09-912-157-2.rsp

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Best: Local Similarity
Matches 88: Conserv
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P47736;
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15-JUN-2002
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                                                                             This SWISS PROTHERLY, is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bloinformatics. Institute. There are no restrictions on its use by non-profit institutions as now as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or.send.an.emil.to-license@ibb.sib.ch).
11- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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PROFELN-TYROSINE PHOSPHAJASE 1.
PROFEIN-TYROSINE PHOSPHAJASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSG0038; ITR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PP; 2.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Cell adhesion; Immunoglobulin domain; Repeat.
SIGNAL.
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IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
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[g_like:
[YR_phosphatase.
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                                                                                                                                                                                                                                         EMBL; M27699; AAA28842.1; -- PIR; B36182; B36182.
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Pfam; PF00047; 19; 2.
Pfam; PF00102; Y_phosphatase; 2.
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PROGOGO, PRILL.
SMOGOGO, FN3; 3.
T. IG_like; 1.
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755
7462 AA;
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Length 1462;

DB 1;

Score 104;

2.6%;

Query Match

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23;
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                                                                                                                                                                                                       259 NDGNDPIQKFFITLQEAGTPTFTKHKDFINGSHTSYILDHFKPNTTFELRIVGKNSIGNG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98010656; PubMed-9346962;
MEDLINE-98010656; PubMed-9346962;
MINATORI H., Mada Y., Tsukamoto N., Maeda M., Kubota H.; Hattori M.,
Iwai K., Minato N.;
"Human SPA-1 product selectively expressed in lymphoid tissues is a specific GTPase-activating protein for Rapl and Rap?.";
J. Biol. Chem. 272:28081-28088(1997).
J. Biol. Chem. 272:28081-28088(1997).
Protein RAP-1A (KREV-1), converting it to the putatively inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 AVAITVPLVVISAFATLFTVMCRKKQQE-----NIYSHLDEES---SESSTYTAALPR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 KSEGROCOOLILKDPROLNSSFKRTGMESOPFLNMKFETDYFVKVVPFPSIKNESNYHPF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 --SG------EVPKVIEEAIYQQNSRNLPYM-------FDKLKTATDYE-- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 FFRTRACDILLQPDNLACKPFW-----KPRNLNISQH-----GSDMQVSF 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 -FRVRACSDLIKE---TCGP-WSENVNGTINDGVAIKPINLSIQCHEDNVIRGNSIAINW 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVPKTPNGKVVSYLIHILGNPMSTVDREMMGPKIRRIDEPHHKTLYESVSPNTNYTVTVS 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 -----KQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALK---PVHSPWAGPIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 -----QNITISQYACHDQV:-----AVTILWSPGALG-IEFLKGFRVILEEL 132
                                                                                                                                                                                                                                                                                                                                                          319 QPTQYPQGITTLSY---DPIFIPKVETTGSTASTITIGHNPPPPDLIDXIQXYELIVSE- 374
11 Similarity .20.0%; Pred. No. 9.4; 88; Conservative 53; Mismatches 136; Indels 164; Gaps
                                                                                                             55 NEGVGPASR-----NSGLYNITFRYD-----NCTTYLNPVGKHVIADA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rubinfeld B., Munemitsu S., Clark R., Conroy L., Watt K., Crosler W.J., McCormick F., Polakis P.; Walseular choing of a Grpase activating protein specific for the Krev-1 protein plinel"; Cell 65:1033-1042(1991).
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Mammalia; Butherla; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
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	703 ISS	592 LESVSSSGTPHKRDSFIYSTWLEDSVSTTSGGSSPGPSRSPHPDAGKLGDPACPEIKIQL 651		RESULT 10	HUMAN STANDARU 79, 013693, 013694	Sec. 1	ABR. Homo sapiens (Human).	Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_Tax10-9606;	r [1] SEQUENCE FROM N.A.	TISSUE-Hippocampus;  MEDLINE-9406546; PubMed-8262969;  Tan F - T Lanna T Manaer E Lim I	The human active breakpoint cluster region-related gene encodes a brain protein with homology to guanine nucleotide exchange proteins	and GTPase-activating proteins."; J. Biol. Chem. 268:27291-27298(1993).	SECULIARY STATE OF 39-859 FROM N.A. (LONG AND SHORT FORMS).	TISSUE-FIOTODIAST; MEDILINE-9335461; PubMed-8349582; Heisterkamp N., Kaartinen V., van Soest S., Bokoch G.M., Groffen J	"Human ABR encodes a protein with GAPrac act DBL nucleotide exchange factor domain."; J. Biol. Chem. 268:16903-16906(1993).	(3) SEOUENCE OF 436		Abk, an active box related gene  Nucleic Acids Res. 17:8821-8831(1989)	EREBT	NATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHO) FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.	-1-TISSUE SPECIFICITY: HIGHLY ENRICHED IN THE BRAIN. MUCH WEAKER EXPRESSION IN HEART, LUNG AND MUSCLE1- SIMILABITY: COMPAINE I DRI-HOMOLOGY (PH) FOMAIN	-i-SIMILARITY: CONTAINS 1 PH DOMAINi-SIMILARITY: CONTAINS 1 C2 DOMAIN.	-!- SIMILARITY: COMTAINS 1 RHO-GAR DOMAIN. -!- SIMILARITY: STRONG, TO HUMAN BCR.	d th	There are no restrictions as its content is i	modified and this statement is not removed. Usage by and for commerc: entities requires a license; agreement (See http://www.isb-sib.ch/annound or early an enail to licenseighteit check.)		EMBL; L19704 EMBL; L19705	Genew; HGN MIM; 60036	InterPro; IPR001008; C2. InterPro; IPR001331; GDS_CDC24.
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•				CC use by non-profit institutions as/long as its content; is it no way CC modified and this statement is notwremoved, visage by and icor commercial CC entitles requires a license agreement; (See hittp://www.ish.sih.n/Annonnocal			DR InterPro; IPRO00331; Rap_GAP.  DR Pfam; PF02145; Rap_GAP; 1	DR FIRM PFOLDES; GOLOCO; 1. DR SIART; SW00390; GOLOCO; 1. KW GTPase activation; Wembrane.	FT DOMAIN 210 397 RAP'RAN-GAP. SQ SEQUENCE 663 Aa; 73391 MM; 3703B7CC603404DA CRC64;	Query Match 2.6%; Score 103.5; DB.1; Length 663; Best Local Similarity 19.5%; Pred. No. 3.4;	Matches 143; Conservative 80; Mismatches 262; Indels 247; Ga	QY 167 MKRETOYFVKVVPRPSIKNESNYHPEFRTRACDLLLQPD	207NIACKDFREEDBAINTCOMCCAMANGERIABBINECTEDENT UVV	71 PLOSPT		VIGDOEHLRLLLRTKCRTYHDVIP		363	226FLGGKVKLQDFKGFRGGLDVTHGQTGTESVYCNFR	KNYK	DD 261 NKEIMFHVSTKLPYTEGDAQQLQRKRHIGNDIVAVVFQDENTPFVPDMIASNFL 314			372 AEYACKAEKPAKLEBRTRAALLETLYEEL-HIHSQSWGGLGGDEDKWENGSGGGGFF	QY 549KGKSGRSLYVAICNHHQFIDEEPDWFEKQFVPFHPPFLR 587	DD 429 ESFKRVIRSRSQSMDAMGLSNKKPNTVSTSHSGSFAPNNPDLAKAAGISLIVPGKSFTRK 488	OY 588 YREPVLEKEDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEA 647	• •		

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Y GTP, THEREBY ACTIVATING
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minidae; Homo.
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23
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PRT; 1275, AA

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16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Guanine nucleotide releasing protein (GNRP) (Ras-specific nucleotide exchange factor CDC25)
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Rominidae; Homo.
NCBL_TaxID-9606;
                                                     STANDARD;
                                                                                                                                                                    (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1275 AA;
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                                                                                                                                                       ASGRF1 OR CDC25
                                                     GNRP_HUMAN
Q13972;
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                        RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 QVTMGHLFOKLASOLGVYKAFVDNYKVALETAEKCSOSNNOFOKISEELKVKGP---KDS 223
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.5%; Score 102; DB 1; Length 859; Best Local Similarity 20.5%; Pred. No. 6.4; Matches 117; Conservative 57; Mismatches 190; Indels 208; Gaps
                                                                                                                                                                                                             factor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                     PELVAVK (IN SHORT ISOFORM).
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(1 761 L -> V (IN REF. 2).
AA, 97696 MM; 9FD50Cnc.
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                                                                                   Pfami, PF00621; RhoGEF; 1.
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(See http://www.lsb-sib.ch/announce,
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                  Wel W., Das B., Park W., Broek D.; *Cloning a 140-kDa brain guanine nucleotide-exchange factor, Cdc25GEF, which regulates the function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5%; Score 101; DB 1; Length 1275; .2%; Pred. No. 13;
                                                                                                                               -1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
-1- SIMILARITY: CONTAINS 1 DEL-MONALONS (PH) DOMAIN.
-1- SIMILARITY: CONTAINS 1 DEL-MONALOGY (PH) DOMAIN.
-1- SIMILARITY: CONTAINS 1 RAS-GEF DOMAIN.
-1- SIMILARITY: CONTAINS 1 RO DOMAIN.
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between the Swiss Institute of Bioinformatics and the El
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2 RAS-GEF.
145381 MW; 86C6F54AAIE45IF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50006; IQ; 1.
PS50003; PH_DOMAIN; 2.
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or send an email to licenseelsb-sib.ch)
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(EDLINE-95129875; PubMed-7828890;
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PR001895; RasGRE_CDC25
PR000219; RhoGEF.
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IPR000048; IQ_region
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                                                                                               Ras,";.
Gene 151:279-284(1994).
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OY 126 RVILEELKSEGROCQOL-ILKD;PROLNSFKRTCHE;SOPFLANKFETDYFVK 176	NIACKPEWKPRNLNISQHGSDMQVS	OY 232 FDHAPHNEGFREFYLHYKLKHEGPFKRKTCKOBOTTETTSCLLONVSPGDYIIELVD 288	OY 269 DŢNTŢRKVMHYALKPVHSPHAGPIRAVAITVPLVVISAFATLFTVMCKKKQQENIYS 345 :	VQCFAYFLQDFCGCEVAL. 4 :: IF: I IEGCEILL. 4	OY 406 DLWEDF:	QY 441KYEVDKKNYKGSGKGELELVA,467   1   1   1   1   1   1   1   1   1	QY 468 VSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHS 527	QY 528 RDHGLQEPGQHTRQGSRRNYFRSKSGRSLX 557 :   :	RESULT 12 RHGG_HUMAN STANDARD; PRR; 974 AA.  (0.43182; 0.4317; 0.971B3; 0.901R81; 0.901R82; DT 15-JUL-1999 (Rel. 30, Created) T16-OCT-2001 (Rel. 40, Last sequence update) T16-OCT-2001 (Rel. 41, Last sennotation update) DE Rho-GTPEAS-activating protein 6 (Rho; type GTPBAS-activating protein DE Rho-GTPEAS-activating protein 6 (Rho; type GTPBAS-activating protein DE Rho-GTPEAS-1.  RAMMALIA: Eutheria; Primates; Catarrini; Hominidae; Homo. OX NCBL_TAXID-9606; DX (1) RND-LINE-2016.206; Pubmed-10599171; RAMEDINE-2016.206; Pubmed-10599171; R *Punctional analysis of ARHGAP6, a novel GTPASS-activating protein for RhoA.; RHDA.; RHDA.; RHDA.; REDINE-98086484; Pubmed-9417914; RX SCURENCE FROM N.A. (ISOFORMS 1 AND 2). RX SCURENCE FROM N.A. (ISOFORMS 1 AND 2). RX BELINE-98086484; Pubmed-9417914; RX SCURENCE ROW defects.; RX Clounds and characterization of a novel region for microphthalmia rith linear skin defects.; RX Clounds and characterization of a novel region for microphthalmia rith linear skin defects.; RX Clounds 46:268-277(1997). CC THEM TO AN INACTIVE GDP-BOUND STAFE. COUNDERING THEM THE ACTIN CYTOSKELFTON.
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Best Local Similarity 18.6%; Pred. No. 9.9;
Matches 178; Conservative 99; Mismatches 294; Indels 385; Gaps 46;
CELL MOTILITY AND SINUTANEOUS RETRACTION OF THE CELL BODY
SCHANDING; THE CELL MORPHOLOCY.
-1- SUBCELLUIAR. LOCATION: CYCOLAGAM.C.
-1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1, 2, 3 (SHOWN HERE), 4 AND 5;
-2- ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL.
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL.
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL.
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL.
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL.
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL.
-1- TISSUE SPECIFICATION.
                                                                                                                                                                                                                                                           PANCREAS AND LIVER.
DISEASE: DEFECTS IN ARHGAP6 MAY BE A CAUSE OF MICROPHTHALMIA WITH
LINEAR SKIN DEFECTS (MLS), A DOMINANT MALE-LEFRAL DISORDER
CHARACTERIZED BY EYE, SKIN AND CENTRAL NERVOUS SYSTEM (CNS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 -----SGLYNITFKYDNCTTYLNPVG-----KHVIADAQNITISQYACHDQVAVTILMS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 POEKSPSG----SFHFD----YEVPLGRGGLKKSMAMDLPSVLAGPASSRSASSILCSSG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 F-----PDNLACKPFWK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGNESQPFLNMKFETDY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 PRNLNISQHGSDMQVSFDHAPHNFGFRFFYL----HYKLKHE------G 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 SLRKKLDSLGKEKNKDKEFIPQAFGMPLSQVIANDRAYKLKQDLQRDEQKDASDFVASLL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 AGGSGRARGADTCGWRMKA------AARPRLCVANEGVGPASRN------------------64
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1 SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF117067; AAF43261.1; --
EMBL; AF177665; AAD53166.1; --
EMBL; AF177665; AAD55087.1; --
EMBL; AF012272; AAC9839.2; --
HSSP; O07960; 1RGP
Genew; HGNC:676; ARHGAP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000198; RhoGAP.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
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2151_MOUSE. STANDARD; PRT; 794 AA.
060821; 060699;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 40, Last annotation update)
210c finger protein 151 (Polyomavirus late initiator promoter binding protein) (LP-1) (Zinc finger protein 213).
2NF151 OR ZFP100.
                                                                                                                                                                                                                                                                                                                                                                                                                                        375 -- CYSS -- -- - RDGQNHMNVQCFAXFLQDFCGCEVALD ME------ DFSLCREG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          762 S---SLRAGPCSLSQG-NLSPNWPRWQGSP------AELDS----- 792
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                                                             SG - 741 | 1 ST 
                                                                                                                                   230 THTTRY WHTTRY WHTTTRY WHITTRY WALL 330
                                                                                                                                                                                                                                                                                        331 3 ----- FFTWORKKQOENIYSHLDE----- ESSESSTYTAALPREKLRPRPKVFL- 374
                                                                                                                                                                                                                                                                                                                                                          423 KHGLQTVGIFRVGSKRRVRQLREEEPRGIDVSLEEEHSVHDVAALLKEFLRDMPDPLLT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 KNYKHKGGGRGSGKGELFLVAVSAIAEKL-------ROAKQSSSAAL---- 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SKFIAVYFDYSCEGD-----VPGILD 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L....STKYRLMDNLPQLCSHL-----HSR-DHGLQEPGQHTRQGSRRNYFRS 550
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                ----OTTETTSCLLQNVSPG------DYITELVDD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596. ENYE: -----ALFWVPPDLQNEVLISLLETDPDVVDYLLRRKASQSSSPDMLQSE 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           645 VSFSVGGRHSSTDSNKASSGDISPYDNNSPVLSERSLLAMQEDAAPGGSEKLYRVPGQFM.704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CBA; TISSUE-Kidney;
MEDLINE-9603919; Pubmed-7575457;
Schulz T.C., Hopwood B., Extraction P.D., Wells J.R.E.;
An unusual arrangement of 13 zinc fingers in the vertebrate gene.
                                                                                                                                                                                                             374 OSRILEALOLSIPAEAQSKKEKARDKKLSINPIYR-----QVPRLVDSCCQHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671 DMPRD----SGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPP 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musiae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Rapp L., Carmichael G.G.;
Submitted (APR-1995):to the EMBL/GenBank/DDBJ databases.
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255, PFKRKTCKOE-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions is not as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AGLGQ------VLEFMYTAKLSLSPENVDDVLAVASFLQMQ-------DIVT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 ACHTLKSLAEPSSTTGESADASAVEGGDKRAKDEKAAATMLSRLGQARGSSSTGPGRELK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 BERGGQAESASSGAEQTEKADAPREPPP--------VELKPDPTSSMA- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 KYRLMDNLPQLCSHL-HSRDHGLQEPGQH-----TRQGSRRNYFRSKSGRSLY 557
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                            -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: FOUND IN ALL THE EMBRYONIC AND ADULT TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-finger; Metal-binding
                                                                                                  -! SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 2.5%; Score 99.5; DB 1; Length 794;
1 Similarity 20.6%; Pred. No. 8.9;
71; Conservative 41; Mismatches 146; Tadele of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFF88E56EDEBF7ED CRC64;
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REGULATES THE EXPRESSION OF SPECIFIC GENES.
                                                                                                                               FINGER PROTEINS.
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ZINC FINGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50097; BTB; 1.
PROSITE; PS00097; BTB; 1.
PROSITE; PS00187; ZINC_FINGER_C2H2_2; 13.
PROSITE; PS50187; ZINC_FINGER_C2H2_2; 13.
Franscription regulation; DNA-binding; Zi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
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C2H2-TYI
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InterPro; IRR600010; BTB_POZ.
InterPro; IPR000822; Znf_C2H2.
Pfan; PR00096; Zf-C2H2; I3.
Pfan; PF00651; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; Znf_C2H2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA85493.1; -
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SMART; SM00355; ZnF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein; Rep
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Best Local S.
Matches 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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207 AABARALSESSBOEMEVEPASKG--EDGQEEGAGPATVKEEGHH-LDNGEPPEENEESA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear, SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-PINGER PROTEINS. ZFX/ZFY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS05157; ZINC_FINGER_C2H2_2; 10.
Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-89168416; PubMed-2493989;
Mardon G., Page D.C.;
The sex-determining region of the mouse Y chromosome encodes
protein with a highly acidic domain and 13 zinc fingers.";
Cell 56:765-770(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 99; DB 1; Length 783;
Pred. No. 9.6;
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                                                                678 IYDSSVPSSELSLP---LMEGLSTDQTETSSLTESVSSSGLGEE 719
                                                                                                              GTDS---GOELGMEGGNLRSGTYGDRTESKAYGSIIHKCEDCGKE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR.
                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                           783 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22H2-TYPE
                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence u
16-COT-2001 (Rel. 40, Last annotation
2. Last annotation
                                                                                                                                                                                                                           PRT;
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InterPro; IPR000822; Znf_C2H2.
Pfam; PP00005; zf-C2H2; 13.
PRINTS; PR00048; ZINCFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88856 MW;
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                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                      ZFY2_MOUSE
P20662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A3149
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SEQUENCE
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210; Gaps .. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 TAALPRE-RLRPRPKVFLC----YSSKDGON---HMNVVQCFAYFLQDFCGCEVALDLWE 409
                                                                                                                                                                                   ELKS----EGROCOQLILKDPKQLNSSFKRTGMESQP--FLNMKFETDYFVKVVPFPSIR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 HSPWAGPIRAVAITVPLVVI---SAFATLFT----VMCRKKQQENIYSHLDEESSESSTY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 DFSLCREGOREWVI----QKIHESQFIIVVCSRGMRYFVDKRNYKHKGGGRGSGKGELFLV 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 TFSDTKEAQQHAVLHQESRTHQ------CS------HCNHKSSNSSDLKRHIISV 633
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                                                            71 TFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSPGALGIEFLKGFRVILE 130
                                                                                                     375 KSKKKRPESKQYQSAIFVAPDGQT -----LRVYPCMFCGKKFKTKRFLK ----RHIK 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512 YRLADNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNWHQFIDEEP 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 NESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFGFRFF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                245 YLHYKLKHEGPFRRRTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPV 304
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WEDLINE-97246296; PubMed-9090055;

GALONIA., D'ANGELO M., Dal Pero F., Sartorello F., Pandolfo D.,
Pallavicini A., Lanfranchi G., Valle G.;
The DNA sequence of cosmid 14-13b from chromosome XIV of
Sarcharomyces cerevisiae reveals an unusually high number of
overlapping open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----RGVNKTCKCKFCDYETAEQTLLNHHLLVVHRKK-----FPHICGECGKGFRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DWFERQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVSAIAEKLROAKOS--SSAALSKFIAVYFDYS-----CEGDVPG-----ILDLSTK
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                      74; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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71-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA decapping protein 2 (PSU1 protein).
DCP2 OR PSU1 OR YNL118C OR N1917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
Matches 117; Conservative
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P53550;
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PSU1_YEAST
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Search completed: May Job time : 22 secs SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation (See http://www.isb-sib.ch/announce, restrictions on DECAPPING IS A THE MAJOR PATHWAY OF MENA DECAPPING ENZYME,
DECAPPING IS A THE MAJOR PATHWAY OF MENA DECRADATION IN

IT OCCURS THROUGH DEADENTLAFION, DECAPPING AND SUBSEQUENT

IT: INTERACTS WITH DORI.

RITH: REFACTS WITH DORI. Query Match 2.5%; Score 99; DB 1; Length 970; Best Local Similarity 17.9%; Pred. No. 13; Matches 106; Conservative 86; Mismatches 182; Indels 218; Gaps 274 LONVSPGDYIIE -- LV ------ DDTNTTRKVMHYALKPVHSPW -- AGPIRAVAITVP 320 419 REWVIOKIHESOPIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVA-VSAI----- 471 :||:: || : ----IFLISGVSEVFNFKPQ 194 -----CEGD 501 --- DHGLQEPGQHTR 540 --MHQFIDEEPDWFE----KQFVPF- 581 --- HPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFC 616 321 LVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALP-----RERLR---- 367 195 VRNEIDKIEWFDFKKISKTMYKSNIKYYLINSMMRPLSMWLRHORQIKNEDQLKSYAEEQ 254 314 OKDOOSSFSSOOOPSIFPSLSEPFANNKNVIPPTMPMANVFMSNPOLFATMNGOPFAPFP 373 |:||: | |:| || || || || ||: ||:| ||: ||:| ||: ||:| ||: ||:| ||: ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| || SIMILARITY: BELONGS TO THE NUDIX HYDROLASS FAMILY. STRONG, TO -----PRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQ rotein is required for mRNA decapping in Saccharomyces and contains a functional MutT motif."; 123 GTESDSWSFPRGKI----SKD----ENDIDCCIREVKE----EIGFDLTD----425 425 P -> L (IN REF. 1) 970 AA; 108667 MW; D53CA2C5A546FA4 161 -----YIDDNQFI-----ERNIQGKNYK----NUDIX BOX. POLY-SER. ----AEKLR--OAKOSSSAALSKFIAVYFDYS PR000086; NUDIX\_hydrolase. 502 VPGILDLSTKYRLMDNLPQLCSHLHSR----138017; PubMed-10508173; 541 OGSRRNYFRSKSGRSLYVAICN----3; NUDIX; 1. 502; NUDIXFAMILY. requires a license a email to license PS00893; NUDIX; 1 feast 13:261-266(1997). S. POMBE SPACI9A8.13 8 drolase. CONFLICT 582 .--368 셤 용 셤 å 셤 à 셤 ò g ð ð 충

429	674	477		
DD 374 FMLPLINNSNSANPIPTPVPPNFNAPPNPMAFGVPNMHNLSGPAVSQPFSLPPAPL 429	617 LKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPR 674	430PRDSGYSSSSPGQLLDILNSKRPDSNVQSSKRPKLKILQRGTDLNSIK 477	675 DSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGIGEEE 720	478 QNNNDETAHSNSQALLDLLKKPTSSQKIHASRPDTSFLPNDSVSGIQDAE 527
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	GenCore version 5.1.4 p5.4578 COPYLight,(C):1993 7 2003 Compuged Ltd.
OM protein - pr	protein search, using sw model
	<pre>(without #alignments) 1616.1819 Million cell updates/sec</pre>
Title: Perfect score: Sequence:	US-09-912-157-2 4013 1 MAPWILQILGSVRFTVNACINGCEADIGCRSYTDELHAVAPL 753
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext, 0.5
Searched:	671580 seqs, 206047115 residues
Total number:of hits sat Minimum:DB seq length::0 Maximum:DB seq length::2	Total number:of hits satisfying chosen parameters: 671580 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	SPTREMBL_21:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

•	095wa7 bulla gould	Q9ay10 Oryza sativ	O9wuf3 mus musculu	088737 mus musculu	Ogdzp6 mus musculu	Osvbs6 mus musculu	P97412 mus musculu	Q91qf8 arabidopsis	015017 homo sapien	019655 caenorhabd1	099pv2 rattus norv	Q8yw]8 anabaena sp	09c0d2 homo sapien	024573 drosophila	O9bhw7 leishmania	O54978 mus musculu	Q9n918 leishmania	096sk7 homo saplen	Q9vqk5 drosophila	09zvd5 arabidopsis	Q9fmd7 arabidopsis	Q9wtr2 mus musculu	1918zl enterococcu	0967x9 tribolium'c	29vu03 drosophila	29vc36 drosophila	28tcu4 homo sapien	Q9n0b3 macaca fasc	09p7q7 schizosacch		
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<b>-</b>	OSUFA0	DOUFAU;	01-MAY-2000	01-MAY-2000.(TrEMBLrel. 13,	Hypothetical	DKFZP434N1928	Homo sapiens (Human)	Eukaryota; Metazoa;	Mammalla, Eutheria,	NCBI_TaxiD#9606; [1]	SEQUENCE FROM N.A.	TISSUE-TESTIS;	Bloecker H., Boecher M., Brandt P., Mewes H.W.,	Wiemann S.;	Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases	EMBL; AL133097; CAB61408.1;	Hypothetical protein	NON_TER	SEQUENCE	Mat	Loca	es	190 H	<del>-</del>	# ′	250 LKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA		61 L	310 G	     121
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370 PKVFLCYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLMEDFSLCREGOREWIGKIHES 429
                          490 IAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFR'549
                                                                                                                                                                                                                                           SSESSTYTAALPRERLRPRFVFLCYSSKDGQNHANVVOCFAYFLQDFCGCEVALDLMED 410 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
                                                                                                       430 QFIIVYCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKF 489
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Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Mus
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar expression to FGF protein (Fragment).
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Nat. Cell Biol. 4:170-174(2002).
EMBL; AF424804; AAL79530.1;
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08R5J8;
01-JUN-2002;
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241 FSLCREGOREWAIQKIHESQPIIVVCSKGMKXPVDKKNPRHKGGSRGEAGGEFFLVAVAA 300
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Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Artinopterygii: Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID-7955;
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                                                                                                                                                                                                                                        531 GLOEP-GOHTROGSRRNYFRSKSGRSLYVAICNMHOFIDEEPDWFEKOFVPFHPPPLRYR
                                                                                                                                                   301 IAEKLRQARQSSSAALRKFIAVYFDYSCEGDVPCSLDLSTRYKLADHLPELCAHLHS
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Tagang M., Friesel R., Kudoh T., Dawid I.;
Tidentification of Sef, a novel modulator of FGF signalling.";
Nat. Cell Biol. 4:165-169(2002).
EMBL, AF364103; AAL76112.1;
SEQUENCE 745 AA, 83431 MW; 56FEIF0B9D98DDB4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 ESVSSSSGLGEEDPPTLPSKLLASGVSR-EHGCHSHTDELQALAPL 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  708 ESVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 753.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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	119 : LEFLKGFRYILEELKSEGROCQOLILKDPROLNSSFRTGMESOPFLANKFETDYFVKVV 178	179 PPPSIKNESKYHPPFERTRACDILIQPDNIACKPFWKPRNIAISQHGSDMQVSFDHAPHN 238  ***********************************	239 FGFRFFYLHYKENEGPFRKRTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMH 298 111 :	299 YALKPYHSEMAGPIRAVAITVPLVVISAFATLFTVWCRKKÕČENIYSHLDEESSESSTYT 358 1 :	(359 AALPREKLRPRYVPLCYSSKDGQNHMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGG 418	419 REWVIQKIHESQFIIVVCSKGMKYPVDKKNYKHKGGGRGSGKGELFIVA 467   1   1   1   1   1   1   1   1   1	468:VSAIAEKLRQARQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHS 527 :	528 RDHGLOEPGOHTROGSRRNYFRSKSGRSLYVALCNMHQFIDEEPDWFEKQFVPFHPPPLR 587   1   1   1   1   1   1   1   1   1	588.YREPVLEKFDSGLVLANDVMCRFQPESDFCLKVEAAVLGATGPADSQHESQHGG 640 :	641 LDQDGEARPALDGSAALQPILHTVRAGSPSDNPRDSGIYDSSVPSSELSLPLMEGLSTDQ 700	7 01 TETSSITESVSSSGIGEEPPALPSKLLSSGS-CKADL 738 :       :	RESULT 5	O9NA64 PRELIMINARY; PRT; 846 A 09NA64; 01-OCT-2000 (TrEMBLrel. 15, Created)	01-OCT-2000 (TrEMBLrel. 1 01-DEC-2001 (TrEMBLrel. 1 Y64G10A:6 protein:		Rhabditidae, Peloderinae, Caer NCBI_TaxID=6239, [1]	SEQUENCE FROM N.A. Ainscough R.;	SUDMICTED [2] SEQUENCE F	none; "Genome sequence o		Query Match 4.2%; Score 170.5; DB 5; Length 846;
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                                                                                                  294 QY-CFEEYEVRLIDSS---GIVMIQSAIITKDELRTE----IINGRPVQFGEF---- 338
                                                                                                                                  159; MESOPFLINKFETDFFVKVVPFPSIKNESNYHPFFFRTRACDLLLØPDNLAC-KPFWKPR 217
                                                                                                                                                       339 ----NFTDIELDTDLIPSVIPIESAHD-----GRC-LCVTENGCSCLAADWRPV 382
                                                                                                                                                                                                                278 SPGDYIIELVDDTNTTRKVMH-YALKPVHSPWAGPIRAVAITVPLVVISAFAIL--FTVM 334
                                                                                                                                                                                                                                                                                      395 LODFCGCEVALDLWEDFSLCREGOREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590 EPVLEKF-------DSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES 636
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                                                                                                                                                                                          218 NLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                         455 GRGSGRGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDV--PGILDLSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
68 kDa type I phosphatidyllnositol-4-phosphate 5-kinase alpha (EC
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ENKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          d. No. 2.5e-06;
Mismatches 225; Indels 211;
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"Type I phosphatidylinositoi-4-phosphate 5-kinases are distinct members of this novel lipid kinase family.";

Eust. (74876; AACS0911.1;

Eust. (74876; AACS0911.1;

Interpro; IPR002499; PIP5K;

Evan; PRO0339; PIP5K; 1.
           562 AA.
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01-DEC-2001 (TrEMBLRel. 19, Last anno
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                            Pred.
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                                         Matches 141; Conservative, 82;
               21.4%;
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321: MDYSLLMSIHNIDHAQREPLSSETQYSVDTR------RPAPQKALYSTAMESIQGEAR 372
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                                                                                                                                                                                                                                    53 VANEGVGPASRNSGLYNITFKYDNCTT-----YLNPVGKHVIADAQNITISQYACHDQV 106
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                                                                                                                                                                                                                                                                                                             1 MASASSGPSS-SVGFSSFDPAVPSCTLSSAASGIKRPMASEVLEARQDSYISLV----- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 DVLMQDFYVVESIFFPSEGSNLTPAHHYNDFRFKTYA------
                                                                         Query Match ( 2.9%; w. Score 117.5; DB. 4; F. Length. 562; Best: Local Similarity 18.1%; Pred. No. 0.098; Matches 133; Conservative 105; Mismatches 239; Indels 257;
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Bukaryota, Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
562 AA; 62633 MW; A8F7988EB73506AO CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last annot
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322 ------VVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALP---- 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                 77, ETILLIPTVALRANMLAKLDVMV---IRYHVWQP-GSKKAAPIVLVSTEAAITLAFKE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 YANRLLQQQRLDRIVIDECHLTLTARSYRRSMMQLAWHVRDVETQTVWLTATLPPIFEDA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363, -- REKLRPRPKVF-----LCYSSKDGQNHMNVVQCF-AYFLQDFCGCEVALDLWEDF 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 FISHNKLTKPLIVRESTNRSNLCYSVRTAEHRMSGMTCYDAVRVD-EBCRARTDIW--- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 ----NGQRD-------RILVYCTS--KELVARLAEMIGCAAXSSESGSEADKAAIIQ 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 SOESGRAGRDGMPAESILLAGPOLDDRAP-ASGRASSAERGRVAPG---ADKEAMQLYRS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611 PESDFCLKVEAAVLGATGPADSQH---ESQHGGLDQDGEARPALDGSAALQPLLHTVKAG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPSDMPRDSGIYDSSVPSSE-LSLPLMEGLSTDQTETSSLTESVSSS---SGLGEEEPPA 723
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GKGELFLVAVSAIAEKLRQAKOSSSAALSKFIAVYFDYSCEGDVPGIL--DLSTKY
                                               Sanchez Alonso P., Guzman P.;
Sanchez Alonso P., Guzman P.;
Sanchez Alonso P., Guzman P.;
Sorganization of chromosome ends in Ustilago maydis: recollike
the lidase moofils at telomeric regions.;
Remis, Arosouss, AAB5264.1;
InterPro, IPR001410. DEAD.
InterPro, IPR001650; Helicase_C.
Pfam: PF00270; DEAD: 1.
Ffam: PF00271; helicase_C:
SNART; SM00440; Helicase_C:
ATP-bluding: Helicase_C:
                                                                                                                                                                                                                                                                                                                        | Similarity 20.4% Score: 117; DB 3; Length 757; Similarity 20.4%; Pred. No. 0.17; Similarity 20.4%; Index 187; Index 190; II; Conservative 56; Mismatches 187; Indexs 190;
Contract of the second
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081789; OLNOV-1998 (TERMELTEL 08, Created)
01-NOV-1998 (TERMELTEL 08, Last sequence update)
01-JUN-2002 (TERMELTEL 21, Last annotation update)
Hypothetical 101.6 kba protein.
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        SEQUENCE FROM N.A.
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Heljnen.L.; Josephys., Edition K.-D;,Judohelsel J;, Jesse T.,
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------KGMKYFVDKKNYKHKG------GGRGSGKGELFLVAVSAIAE-----K 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572 IYIYSLAHVVQGVKKVLHKKKFSSPICSASTFYGTSGVG---LTLVFTDGTVEIRSLPE 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GPASR-----NSGLYNITFKYDNCTTYLNPVGKHV---IADAQNI--TISQYACHDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AEGKASRVYVIGSSSNSLQVVLLNEQTETRMIKLGLHVSEPCADMEMIIADVNEQSKHKQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 VAVTILWSPGALGI--EFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELEVIGESGRAYAAYDDYMIERYLIQSQSKSSPSLPKETVVKLPPSDSSSITVGKFLTNP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 --FLIMKEETDY-----FVKVVPFPSIKNESN---YHPFF-----FRTRACDLLLQPD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 SHILNLSDE-DYAQLAKDAVPFLPFHTVPKESSRSAHFPGFTKVKNVYITGHCDGTISVW 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE THE THE STATE OF THE STATE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 LTENSFIPPQGSLKKGNHIVQSVKYIKLTGSITCIQKSQNSKHLAIGSDQGHDSLVEVI 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...-----VMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRFKVFLCYSSKD 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 GONHMINVYQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCS--- 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GK----TVEEISIRQPSVLVCSEKA 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.9%; Score 117; DB 10; Length 917;
Best Local Similarity 18.3%; Pred. No. 0.23;
Matches 167; Conservative 130; Mismatches 296; Indels 320;
                                                                                                                                                                                                                                                                                                                                                             Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein; Repeat; WD repeat; 917 AA; 101552 MW; 1809BDC42302C820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/Genbank/DDBJ databases
--- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS)
EMBL; ALG1135; CAR20026:1; THE
eurosids II) Brassicales; Brassicaceae; Arabidopsis.
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Pfam; PF00400; WD40;
Hypothetical protein; Repeat; WD
SEQUENCE 917 AA; 101552 MW;
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### COLUMN N. P.	PRELIMINARY, PRT, 2946 AA.  PROCEDURE.  PROCEDURE.		8	
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### STREETH   1988   1998   19	### STEENESSS 714  **PARSESSE 91  **PRELIMINARY, PRT: 2346 AA.  **PROCEDING	:   :   :   :	ੱ <u>ਨੂੰ</u>	523 523
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004001 WD4013. 0040019 WD4019.	004001; WD40; 3. 00400018; WD40; 3. 0050018; WD40; 3. 0050018; WD40; 1. 00550094; WD40; 2. 00550094; WD_REPEATS_REGION; 1. 005	•	! ` <del>2</del>	1075
PD00018; WD40; 1.  #D001018; WD40; 1.  #D001018; WD40; 3.  #D001018; WD40; 3.  #D001019; WD40; 3.  #D001010; WD40; 3.  #D0101010; WD40; 3.  #D0101010; WD40; MD40; MD401010; MD40; MD401010; MD40101010; MD40101010; MD40101010; MD4010101010; MD401010101010101010101010101010101010101	Name	i	<u></u>	
09KE0 PS50197; BEACH; 1. PS50197; BEACH; 1. PS50194; WD_REPEARS_2; 1. PS50294; WD_REPEARS_2; 1. PS50294; WD_REPEARS_2; 1.  To repeat. 2946 AA; 321930 MW; B162CFBDEB5D3372 CRC64; DT 2946 AA; 321930 MW; B162CFBDEB5D3372 CRC64; DT 294; Score 117; DB 10; Length 2946; GN 4; Conservative 105; Mismatches 314; Indels 294; Gaps 40; OC COLCSVFTVNACIMOSQIAVAAGGSGBARGADTGGWRMKAAARPRICVANEGYGPA 61 OX	99KE0 PS501921; WAG0: 3. PS50194; WB_REPEATS_2: 1. PS50194; WB_REPEATS_2: 1. PS50194; WB_REPEATS_2: 1. PS50194; WB_REPEATS_2: 1.  TO PS50194; WB_REPEATS_2:	1. BEACH;	. RE	SULT 10
PS50082; WD_REPEATS_2; 1.  PS50094; WD_REPEATS_2; 1.  ND_repeat. 2946_AA; 321930 MW; B162CFBDEB5D3372 CRC64;  2946_AA; 321930 MW; B162CFBDEB5D3372 CRC64;  Conservative 117; DB 10; Length 2946;  Similarity 18.74; Pred. No. 1.4;  Conservative 105; Mismatches 314; Indels 294; Gaps 40;  COCCOVETVWACLANGSQLAVAAGGSGBARGADTGSWRMKAAARPRICVANEGYGPA 61  OX	PS50082; WD_REPEATS_2; 1. PS50094; WD_REPEATS_2; 1. PS50194; WD_REPEATS_REGION; 1.4; PS50194; WD_REPEATS_REGION; WD_REPEATS_	M00320; W	<u>6</u> 6	KE04
#D repeat.  2946 AA; 321930 MW; Bi62CFBDEB5D3372 CRC64;  2946 AA; 321930 MW; Bi62CFBDEB5D3372 CRC64;  51	#D repeat.  2946 AA; 321930 MW; Bi62CFBDEB5D3372 CRC64;  2946 AA; 321930 MW; Bi62CFBDEB5D3372 CRC64;  Similarity 18.7%; Pred. No. 1.4;  4; Conservative 105; Mismatches 314; Indels 294; Gaps 40;  COLCSVETVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRICVANEGYGPA 61  COLCSVETVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRICVANEGYGPA 61  RN  RN  RN  RN  RN  RN  RN  RN  RN  R	PS50082; WD_REPEATS_2; 1. PS50294; WD_REPEATS REGION:	181	•
Similarity 18.7%; Score 117; DB 10; Length 2946; GN 68.7%; Pred. No. 1.4; GN 68.4; Conservative 105; Mismatches 314; Indels 294; Gaps 40; OC CLOLCSVFTVNACLNGSQLAVAAGGSGBARGADICGNRMKAAARPRICCVANEGVGPA 61 OX	Similarity 18.7%;   Pred. No. 1.4;   Ganstant 18.7%;   Pred. No. 1.4;   Ganstant 18.7%;   Pred. No. 1.4;   Ganstant 105;   Mismatches 314;   Indels 294;   Gaps 40;   OC CLESVETVNACLNGSOLAVAAGGSGRARGADTCGWRMKAARPRICVANEGVGPA 61   CONTROL   CONTR	WD repeat. 2946 AA; 321930 MW;	20.0	
00 00 0X	61 0X	2.9%; Score 117; DB 10; Length 2946; Similarity 18.7%; Pred. No. 1.4; Conservative 105; Mismatches 314; Indels 294; Gans	O C C	Transp BH1054 Bactll
	THE STATE OF THE S	. 19	88	Bacill NCBI_T

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PHDNEIGFDLPGPDGN---SVEDDNVGSLNVPESVRQEKEHG------1035
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                                                                                       RNSGLYNITERYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIEF 121
                                                                                                                                                               TARREST SADNOGIENTERA COLOR A 67
                                                                                                                                                                                                                                                                             ESQPELMMKEETDYFVKVVPEPSIKNESNYHPEFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HI-FITTO TO A COMPONENT OF THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q--PDNIACKPEWERPRNINISQHGSDMQVSFDHAPHNFGFREFYLHYRLKHEGPFKRKT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMGPVYIFKEPIGPERMARLASRGGDVLPCFGNGA---GLPWIATANDIVRN----- 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOEOTTETTS-----VMHYA-- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KABESSILDADIGGYTHLIXHPCLLSGRFCPD--ASLSGAAGTLRRPAEVLGQVHVATR 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CRKKQQE---NIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRONNEELCRYQGPEILARILSYLLHSLASLDRKHDGYGEBEL-VAAIVSLCQSQK--IN 786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESGFIIVVCSKGMK-- 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLKVQLFRTLLLD-----LKIW---SLCNYGLQKKLLSSLQDMVFTEATAMRDAEAI 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----YFVDKKN----YKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAA- 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNL--PQLCSHLHSRDHGLQE----PGQH 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRRILIGFIIDSPQPHQVARVLHLMTRLVVQPHAARAQMFAEVFITSGGIETLLVLLQRE 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDS 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTGEDNVLAMGRSGKR-----SSTDPSEKS--PYN-----ESGSVKQLDS 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLNDV-MCKPGPESDFCLKVEAAVLGATG-PADSQHESQHGGLDGDGEARPALDGSAA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGL 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus halodurans...
Bacterla: Firmicutes; Bacillus/Clostridium group; Bacillales;
Bactlaceae; Bacillus.
[1]
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-2000 (TrEMBLrel. 15, Last sequence update)
-2002 (TrEMBLrel. 21, Last annotation update)
osase (08)/ABC transporter (ATP-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOYNVDNSDAVVVGIIRLIGALISSGHLÆFDFDARS 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---EEPPA------LPSKLLSSGSCKADLGCRS 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥ 8
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01.JUN-2002 (TrEMBLrel. 21, Last annotation update) Protein kinase (Fragment).
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Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01404; EPH lbd; 1
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00060; FN3; 2.
SMART; SM00454; SAM; 1.
SMART; SM00219; TYFKG;
                                                                                                                                              NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY-ACHDQVAVTILWSPGALGI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCF---AYFLQDFCGCEVALDLWEDFSLCREGOREWV----IQKIHESQFIIVVCSKGMK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 EFLKGFRVILEELKSEGR------QCQQL--ILKDPKQLNSSFKRTGMESQPFLNMKF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 ETDYFV-----KVVPF-PSI-----KNESNYHPFFFRTRACDLLLQPDNLACKPFWKPR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EELKAKOHOKLK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 NINISQHG-----SDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTET 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 ISCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVIS-AFA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 -----ESVHIELGLVALAHNLR 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 TLFTVMCRKKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525 KRATVDRRSKEPKNINQHKNREN------RIKRF------SKRFYVL 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 YFVDKKNYKHKGGGRGSGKGELFLVAVSAI------AEKLRQAKQSSSAALSK 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613 MFIEKGEMVGLLGPNGAGKSTTISMISSLIQPTSGDVLLKGGSIHKQSKAIRSILGVVPQ 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIAVYFDYSCE-----GDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.9%; Score 116.5; DB 16; Length 901; Best Local Similarity 19.6%; Pred. No. 0.25; Matches 112; Conservative 76; Mismatches 169; Indels 215;
                                                                                                                                                                                                                                                                                                                                                                                           // Transport; Complete proteome.
901 AA; 104585 WW; E519406E650B2CBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 ARDFKVYECESCEGCPFKPECTKARGNRQVHYNPVY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           938 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 SRRNYFRSKSGRSLYVAICNMHQ --- FIDEEP 571
                                                                                                                                                                                            (ABC TRANSPORTERS).

EMBL; AP001510; BAB04773 1; -
Interpro; IPR003593; AAA_ATPase.
Interpro; IPR003439; ABC_transport.
Interpro; IPR002559; Transposase_11.
                                                                                                                                                                                                                                                                                          Pfam; PF00005; ABC_tran; 1.
Pfam; PF01609; Transposae_11; 1.
Probom; PD000006; ABC_transportr; 1.
PROSITE; SM0382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              060669;
01-NOV-1996 (TrEMBLrel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Q60669
ID Q60669
AC Q60669
DT 01-NOV
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188 -----NETSLILEWSEPRDLGGRDDLLYNVICKKCRGSSGAGGPATCSRCDDNVE 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 FVPROLGLIERRYHIS----HLLAHIRYIFEVQAVNGVSGKSPLPPRYAAVNITINQAA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 PDNLACKPFWRPRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPF-KRKTCKQ 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 VANEGVGPA-----SRNSG------LYNITFKYDN------CITYLNPVGKHVIADAQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 KAKGGEGPCLPCPPNSRTTSPAASICTCHNNFYRADSDSADSACTTRRSP-PRGVISNV-
145 KDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.9%; Score 115.5; DB 11; Length 938; Best Local Similarity 19.4%; Pred. No. 0.33; Matches 160; Conservative 120; Mismatches 285; Indels 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIL KINASE_ATP; 1.
PROSITE; PS00110; PROTEIN KINASE_DOM; 1.
PROSITE; PS007109; PROTEIN_KINASE_TR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
Glycoprotein; Kinase; Phosphorylation; Receptor; Repeat; Transmembrane; Tyrogine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVFFTVNACL-NGSQLAVA----AGGSGR---ARGADTCGWRMKAAARPRLC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      938 AA; 103997 MW; 8D128CA46F19E73F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:104770; Ephb3.
InterPro; IPR001090; Ephrin_receptor.
InterPro; IPR001090; Ebhrin_receptor.
InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003961; FN_III.
InterPro; IPR001601; SAM.
InterPro; IPR001405; YAR.
InterPro; IPR001405; YAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam. PF00536; SAM; 1:
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
ProDom; PD0000001; EUK_PKinase; 1.
ProDom; PD001495; EPhrin_receptor; 1.
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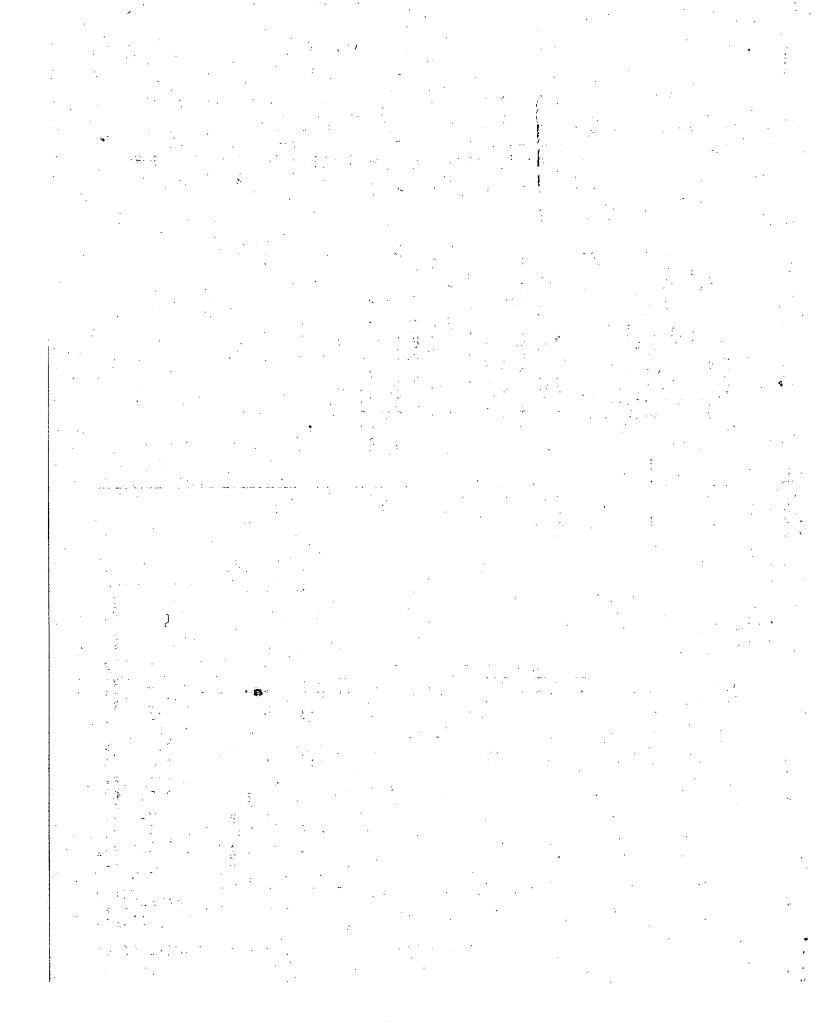
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	173-YFVKVVPEPS:IKNESNYHPFEFTRACDLLLQPDNIACKPFWRPRNLNISQHGSDM 228   1: :       : :       : :		268:ETTSCLLQNVSPGDYIIELVDDTNTTRKVHHYALKPVHSPWAGPIRAVAITVPLVVISAF 327  190'FLQKLLPGYYM***		GQNHMNVVQCFAYFLQDF-CGCEVALDLWEDFSLCREGOREWVIQKIHESQFII	VVCSKGMKYEVDKKNYKHKGGRGSGKGELFLYAVSALAEKLKQ  ! : A!	478AKOSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLFQLCSHL-HSR 528   367 DDHWGGIPARNSKGERLLLXIGIIDILQSYRFVKKLEHSWKALVHDG 413	529 DH-GLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWPEKQFVPFHPPPLR 587	588 YREPVLEKFDSGLVLNDVMCKFGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEA 647	648 RPALDGSAALQPLLHTVRGSPSDMPRDSGIVDSSVFSSELSLPLMEGLSTDQTET 703  -   :-    :-	704 SSLTESY 710	ob 534 Syrleki 540 RESULT 13	0 094460 PRELIMINARY; PR7 094460; 01-MAR-2001 (TEMBLEEL: 16, Creat 01-WAR-2001 (TEMBLEEL: 16, Last	01-JUN-2002 (TrEMBirel. 21, Last annotation update) BA425A6.2 (Similar to connexin) (Fragment). BA425A6.2.	Homo Sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhin1; Hominidae; Homo. NCBI TaxID-9606;	SEQUENCE FROM N.A. Heath P.:	SUBDITEC (AFF.2009) to the MBL/Ocmbank/DDD databases. EMBL: AL121749; CAC10186.1; InterPro: IFR005500; Cannexin.			· •
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Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Deccher M., Bloccker H., Bauerasches S., Blum H., Duesterhoeft A., Roper A., Koehrer K., Strack N., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,

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652 DGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVP---SSELSLPLMEGLSTDQTETSSLTE 708
                                                                                                                                                         600 LVLNDVMC------KPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 DGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVP---SSELSLPLMEGLSTDQTETSSLTE 708
                                  Indels 25; Gaps
                                                                     600 LVLNDVMC------KPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siberger J., Soehl G., Willecke R.;
"Structural and functional diversity of connexin genes in the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
       Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and human genome.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ414564; CAC93846.1;
InterPro; IPR000500; Connexin.
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PROSITE; PS00407; CONNEXINS_1; UNKNOWN_1.
PROSITE; PS00408; CONNEXINS_2; UNKNOWN_1.
SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;
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Last annotation update)
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Query Match 2.8%; Score 111.5; Best Local Similarity 28.9%; Pred. No. 0.17 Matches 43; Conservative 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 EPIMLPPPLELGYRVTVEDLDREKEAARQRINSALQVEDKAISDCRPSRPSH---TLSSL 267
                                                                                                                                                                                                                                                                                                                                                                                                             474 KLRQAKQSS-SAALSKFIAVYFDYSCEGDVPGI------LDLSTKYRLMDNLPQ 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            521 LCSHLHSRDHGLQE--PGQHTRQGSRRNYFRSKSGRSLYVAICNWHQFIDEEPDWFEKQF 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       579 VPFH-PPPL------RYREPVLEKFDSGLVLNDVM---CKPGPESDFCLKVEAA 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 ATGASGLPAVSKAPS----MDAQQETHKSODCLGLLDPLASA--AGVPSTAPMSGKKHRP:321
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                                                                                              Mewes H.W., Ottenwaelder B., Obermaler B., Tampe J., Heubner Manbutt R., Korn B., Klein W., Poustka A.;
"Towards a Catalog of Human Genes and Proteins: Sequencing an Analysis of 500 Novel Complete Protein Coding Human CDNAs.";
Genome Res. 11:422-435(2001).
EMBL; ALI17401; CAB55902.2;
                                                                                                                                                                                                                                                                                                             2.7%; Score 110; DB 4; Length 428; 23.5%; Pred. No. 0.31; 1ve 42; Mismatches 108; Indels
                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 428 AA; 45443 MW; FA75BAClA3FDB3EE CRC64;
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Title: US-09-912-157-2	39 92.5
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## SUMMARIES

Result No.						
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424	Score	Match	Match Length	60	TD.	Description
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~	312	7.8	998	m	US-09-022-255-10	10,
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10	306	7.6	864	٣	US-09-022-255-2	7
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13	116.5	2.9	666	*	US-09-192-435-1	÷
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77	115	2.9	966	~	US-08-449-645A-20	20,
22	115	2,9	866	N	US-08-702-367A-20	20,
23	115	5.9	966	S	PCT-US95-04681-20	20,
77	113.5	7.8	617	4	US-09-188-930-303	303,
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56	66	2.5	595	~	US-08-376-843-3	'n
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                                                                                                              69 NITERYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKG 439
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                                                                                                                                                                                                                                                                                                                                         173 YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL-----
Best Local Similarity 23.1%; Pred. No. 1.9e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146;
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APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 607203361 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
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Patent No. 6072033
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51 University Street
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69 NITERYDNC--TYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS 113
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                                                                                                                                                                                                                                                                                                                                        FILING, DATE: 7 AGGIST 1995,
PRIOR, APPLICATION, DATE: 7 APPLICATION, DATE: 3 NARCH 1995
FILING DATE: 23 NARCH 1995
ATTORNET AGENT INFORMATION: NAME: Perkins, Perticia Anne REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELEPHONE: (206)587-0430
SYSTEM: Apple Operating Sy
Microsoft Word for Apple,
                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
**APPLICATION NUMBER: USSN 09/620,694
**FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
                                                                                                   APPLICATION NUMBER: US/09/022,255
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549 RSKSGRSLYVAICNMHQFIDEEPDWFE--
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                                  SOFTWARE: Microsoft W. CURRENT APPLICATION DATA
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OY 114PGALGIEFLEGFRVILEELKSEGROCOOLILKDPROLNSSFKRTGMESOPFLNNKFETD 172   1   1   1   1   1   1   1   1   1	OY 173 YPVKV,-VPFPSIKNESNYHPFPFRTRACDLLLQPDNLACKPFWKPRNL 219	220INSOHGSDMOVSFDHAPHNFGFRFYLHYKLKHBGPFRRKTCKOBOTTETT	OD 210 OLKVSFTLANDESFRIQILLITSFFHAENHSCFEHRH-HIPPAKKEEFHQKSNVTLKIKNIN 2/9  Qy 211 SCLLQNVSPGDXIIELVDDTNTTRKVMHYALKFVHSPRÄGPIRAVAITVPLVVISAE 327	275 GCCRHQVQIQPPFSSCLNDCLRHSATVSCPEMPDTPEPIPDXWPLWYWFITGISILLVG	QY). 328 ATLETVMCRKRQGENISHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQN 383  G PART   G	384 HMNVQCEAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKG	SECRETARY OF THE SECOND	440.AVV 4.0.AVV KRYDDKRYKHKGGG-7RGSGKGELFLVAVSAIABKLRQAKGSSSAALSKFIA	451 TRAKMOALLGRGABVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYVV	OY 492 VYE-DYSCEGDVPGILDLSTKYRIMDNLPOLCSHLHSRDHGLQEPQQHTRQGSRRNYF 548	549 RSKSGRSLYVAICHMHQPIDEEPDWFEKQFVPPHPPPLRYREPVLEKFDSGL	5-11   1   1   1   1   1   1   1   1   1	OY 601 VLANDWICKEGESSFECLKYEAAVLGATCPADSOHESQHGG 640	DD 618 VKRAPLVRE:PGSQACLAIDPLVGEEGGAAVAKLEPHLQPRGQPAPQPLHTLVLAAEEGA 676	641 LDQDGRARPALDGSAALQPLLHTVKAGSPSDWPRDSGIYDSSVPSSELSLP	677 LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPGAGRNSVLF-	OY 692 LABGLSTDQTETSSLIESYSSSGLGEEEPPAARSKLLSSGCKAALGG /40 Db 728 L-GSSTPHASPDLIEDVFERLEGLALSLEDGSGGGG 768		RESULT 4 US-08-973-4 Sequence 4. Aprolication HS/0807873	o. 6083906 INFORMATION:	; APPLICANT: Troutt, Anthony ; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production	; NUMBER OF SEQUENCES: 4 ; CORRESPONDED ADMINISTRATION OF THE SECOND OF	Seattle	STATE: WA STP: GARDI	ER READABLE FORM: UM TYPE: Floppy dis) UTER: Apple PowerMad	<pre>p OPERATING SYSTEM: Apple Operating System 7.5.5 software: Microsoft Word for PowerMacintosh, Version 6.0.1</pre>	NE I	CLASSARTICATION: 530	
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Db 560 RSPGGRQLRAALDRERDWQVRCPDWFECENLIFSADDQDAPSLDEEV-FEEPLLPP-GTGI_617  Qy 601 VLANDVACKPGPESDFCLKVBAAVLGATGPADSQHE	618 WRAPLVRE-PGSQACLAIDPLYGEBGGAAVAKLEPHLQPRGQPAPQPLHTLVL	UY 04.1 HIGH PARAMASAN TALAITTI PELAHVYASAN SANAYAN SEELSEN 691 Db 677 LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPGAGRNSVLFLFVDFEDSP 7.27	QY 692 IMPGLSTDQTETSSVSSSQLGEEEPPALPSKLLSSGSGKADLGC 740			; Patent No. 6072037; GENERAL INFORMATION:	APPLICANT: Yao, Zhengbin APPLICANT: Springs, Melanie APPLICANT: Panelog, utilian	£ 55	CORRESPONDENCE ADDRESS: ADDRESSEE: Immunex Corporation	; STREET: 51 University Street; ; CITY: Seattle ; STATE: WA	; COUNTRY: USA ; 2IP: 98101	< Q	COMPUTER: Apple Power Macintosh ; OPERATING SYSTEM: Apple Operating System 7.5.5 ; SOPERATING SYSTEM: Apple Operating System 7.5.5	LEATION DATA DE SEPTE, VELSION OF SEPTEMBER ON NUMBER OF SEPTEMBER OF	FILING DATE: 05/05/02/030	FAIOR APPLICATION DATA: APPLICATION NUMBER: 08/620,694	FILE DATE  CLASSIFICATION: PRIOR APPLICATION DATA:	# APPLICATION NUMBER: USSN 08/410,535 # FILICH DATE: 23 MARCH 1995	CHASSIFICATION: TATORNEY/AGENT INFORMATION: NAME: Perkins, Patricia Anne	REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2617-B	일;;	TELEFAX: (206); INFORMATION FOR ID NO: 10: SENTING CHARALTERITY	LENGTH: 866 amino acids	TOPPLOCY: Linear MOLECULE TYPE: protein US-09-022-696-10	7.8%; Score 312; DB 3; Length 866; Llarity 23:1%; Pred. No. 1.9e-23;	Matches 1/8; Conservative 107; Mismatches 338; Indels 146; Ga	OY OS NITERIDACTYLLNPVGKHVIADAQNITISQYACHDQVAVIIJWS 113		

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728 L-GSSTPMASPDLLPEDVR

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FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
                                                                                                                        NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623
TELECOMMUNICATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                               TYPE: amino acid arrough: Popology:
                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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100 LOTDASILYLEGAELSVLOLNTNERLCVR--FEFLSKLRHHHRRWRFTFSHFV-VDPDOE 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.8%; Score 312; DB 3; Length 866; Best Local Similarity 23.1%; Pred. No. 1.9e-23; Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK-;-PFWKPRNL-;---
                                                                                                       APPLICANT: Yao: Zhengbin
APPLICANT: Springs, Melanie...
APPLICANT: Springs, Melanie...
APPLICANT: Fanslow, William
TILE OF: INVENTON No. 609630561 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: MICTOSOft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: SUSSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JMBER: US/08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/022,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                      Sequence.10, Application US/09022253
Patent.No: 6096305
                                                                                                                                                                                                                                                E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: U
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RESULT 5
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                                                                    328 ATLETVMCRKKQGENIYSHLDEESSESSTYTAALPRERLRPRP----KVFLCYSSKDGQN 383
                                                                                                | :: | | | :: | | | 618 | ... | | 618 VKRAPLVRE-PGSQACIAIDPLVGEGGAAVAKLEPHLQPRGQPAPQPLHTLVLAAEEGA 676
                          275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLWYWFITGISILLVG 334
                                                                                                                                               HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGOREWV----IQKIHESQFIIVVCSKG: 439
                                                                                                                                                                                                                                             VYF-DYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG--SRRNYF 548
                                                                                                                                                                                                                                                                                                                                                                    549 RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL 600
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271 SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
                                                                                                                                                                                                                       440 MKIFVDRKNYKHKGGG------RGSGKGELFLVAVSAIREKLRQAKOSSSAALSKFIA 491
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APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, Milliam
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
WINBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
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FILING DATE: 23 MARCH 1995
CLASSIFICATION:
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51 University Street
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APPLICATION NUMBER: 08/620,694
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APPLICATION NUMBER: US
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MEDIUM TYPE
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Query Match 7.8%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.9e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps
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*NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 5.2617-B
TELECOMOUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHRACTERISTICS:
LENGTH: 866 anino acids
TYPE: anino acid
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
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RESULT 7 US-09-022-259-10

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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 SCLLQNVSPGDYIIELVDDT----NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 7.8%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.9e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 NITFRYDNC - - TYLNPVGKHVIADAQNIT -----ISQYACHDQ -----VAVTILWS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLWYYWFITGISILLVG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRP----KVFLCYSSKDGQN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL-----
                                                              priggs, Welanie
anslow, William
NTION: No. 6191104el Receptor That Binds IL-17
UENCES: 10
                                                                                                                                                                                                                                                                                                                                                                             YSTEM: Apple Operating System 7.5.5 Microsoft Word for Apple, Version 6.0.
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APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/022,259
                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 2617-B
Application US/09022259
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APPLICATION NUMBER: 08/620,694
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MATION NUMBER: 34,695
                                                                                                                                                                                            3: Immunex Corporation 51 University Street
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SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT, APPLICATION DATA:
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                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex C
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                       APPLICANT: Fanslow, 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                              Seattle
                                                                                                                                                                                                                                                                          USA
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601 VLNDVMCKPGPESDFCLKVBAAVLGATGPADSQHE-------SQHGG 540
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335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSA-DHPL 390
                                                                                         492 VYF-DYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTRQG--SRRNYF 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDQDGEARPALDGSA---ALQ----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKG 439
                                                                                                                                                                                                                                                                                                                                                                                         549 RSKSGRSLYVAICNNHOFIDEEPDWFE-----KOFVPFHPPPLRYREPVLEKFDSGL 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                560 RSPGGROLRAALDRFRDWOVRCPDWFECENLYSADDQDAPSLDEEV-FEEPLLPP-GTGI 617
                                                                                                                                                                   440 MKYFVDKKNYKHKGGG------RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIA 491
                                                                                                                                                                                                                        451 TR----AKWOALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKR-----PACFGTYVV 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSKSCQAQGGC 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             692 LMEGLSTDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSCKADLGC 740
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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342 IICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPR-KVWIVYSA-DHPLYVEVVLK 399
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                                                                                                                                                                                                                                                                                                                                                                                                                         173 YEVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL----- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 SCLLONVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 SVILLIVCHTWRLAGPGS---EXYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSA-DHPL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548
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                                                                                                                                                                                                                                                                                                                                    114 y-PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQPFLNMKFETD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEEFHQRSNVTLTLRNLK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 GCCRHOVOIOPFFSSCLNDCLRHSATVSCPENPDTPEPIPDYNPLAVYWFITGISILLVG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 ATLETVMCRKKQQENIYSHLDEESSESTYTAALPRERLRPRP----KVFLCYSSKDGQN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600
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                                                                                                                                                   Query Match
Best Local Similarity 23.1%; Pred. No. 1.9e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146;
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CHARACTERISTICS:
866 amino acids
                                                                                       MOLECULE TYPE: ...protein
                                                amino acid
                                                                      linear
                                                                                                             US-09-022-257-10
                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-620-694A-2
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--LILKOPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRAC '199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 CFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPF-FSSCLND-----CLR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 QNVSPGDYIIELVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match.
Best Local Similarity 22.5%; Pred. No. 8.2e-23;
Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 GWRM------KAMARPRL-----CVANEGVGPASRNSGLYNITFRYDNCTTYLNPVGR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 GWLLILLINVLAPGRASPRILDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNI 76
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                                                                                                                                                                                                                                           OPERATING SYSTEM: Apple Operating System 7.5.5 SOPTWARE: Microsoft Word for Apple, Version 6.0.1. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          US/08/620, 694Ac
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN .08/538,765
FILING DATE: 7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
                                                                                                                    STATE OF STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Perkins, Patricia Anne. REGISTRATION NUMBER: 34,695
i: Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: :435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                              ·USA
                                                          Seattle
                                                                                                                                   98101
   ADDRESSEE:
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                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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391 FAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQK----IHESQFIIVVCSKGMKYFVDK 446

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A CONTROL OF THE STATE OF THE S	TOPOLOGY: % Ilinear shall was by the property of the property	Query Match SAGE 2.5%, ASCORE.306; DB 3; Length,864; Best Local Similarity 22.5%; Pred. No. 8.2e-23; Matches 189; Conservative 128; Mismatches 319; Indels 203;	CONSTRUCTOR CONTROL CO			Db- 132 LSMLQHHRKRWRFSF-55; SHFYYDPGQBYBYYVHHLRKPIPDGDPNHKSKIIFYK Qy 200 DLLLQPDNLACKPFWKPRNLNISQHGSD	186	DD 245 CEDVVKQIFAPRQEEFHQRANVIFILSKFHWCCHHHYQYQPF-FSSCLND	Db 297 HAVTVPCPVISNTTVPKPVADXIPLMVYGLITLIAILLVGSV\ Oy 331 FTVMCRKKQQENIYSHLDEESSESSYTAALPRERLRPRPRVFLCYSSKDGONHMVVV	342	Qy 391 FAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQRIHESQFIIVVCSKGMKYFY	447	497 SC-EGDVPGILDLSTKYRLADNILPQLCSHLHSRDHGLQEPGQH	510	Db 568 RQLKEAVLRFQEWOTQCPDWFERENLCLADGQDLFSLDEEVFEDPLLPP-GGGIVKQC Qy 607 CKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGF	DD 627 VRELP-SDCCLVVDVCVSEEESRWAKLDPQLWPQRELVAHTLQSMVLPA	678	QY 693MEGISTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTU :: :: :	ά. 	; Sequence 2, Application US/09022696 ; Patent No. 6072037 ; GENERAL INFORMATION: ; APPLICANT: You. Zhenobin	٠.,
	454	509	553	606 626	648 677	692 734										:			\ 		
	01	QSSSAALSKEIAVYEUY   ::     PACFGTYVVCYFSG			MPORELVAHTLQSMVLPAEQV						eptor That Binds IL-17			System 7.5.5 , Version 6.0.1							
	400 PAOPLITACGTEVALDILIEBQVISEVGYWTWYSRQKQEMVESNSKIIILCSRG	455 AKWAILGWAEPAVOLRCDHWRPAGDLFTAANNILEPEKR	497.SC-EGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSG               : ::::         : :   :	554 RSLYVAICHAHOPIDEEPDMFEKQFYPFHPPPLRYREPVLEKFDSGLVLNDVM 	607, CKPQPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEAR	649 PALDGSAALQPLHITVRAGSPSDMPRDSGIYDSSYPSSELSLPL	693MEGLSTDQTETSSLTESVSSSGLGBEEPPALPSKLLSSGSCKADLGCRSYTDE ::	RESULT 10 0S-09-022-255-2	Sequence 2, Application US/09022255 Patent No. 6072033 GENERAL INFORMATION:	APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Welanie APPLICANT: Fanglow William	TITLE OF INVENTION: No. 607203391 Receptor T. NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:	ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle	COUNTRY: USA ZIP: 98101 COMPUTER READABLE FORM:	disk r Macintosh ple Operating Sy Word for Apple,	RRENT APPLICATION DATA: APPLICATION NUMBER: US/09/022,255 FILING DATE: CLASSIFICATION:	PRIOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/620,694 PILING DATE:, 21 MARCH 1996	APPLICATION NUMBER: USSN 08/538,765 FILING DATE: 7 AUGUST 1995 PRIOR APPLICATION DATA:	APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995 ATTORNEY/AGENT INFORMATION:	5885	TELEPHONE: (206)587-0430 TELEFAX: (206). INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:	LENGTH: 864 amino acids TYPE: amino acid
		a d	, q qa	OX,	γο	à a	à a	RESULT 10 US-09-022	; Sequ ; Pate	4 4 4	:⇔≅ŏ 					<u>αί</u>	<u></u>		F	; INF	

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D------HAPHNFGFRFFYLHYKLKHE---GPFKRKTCKQEQTTETTSCLL 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSPGDYIIELVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVALTVPLVVISAFATL 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // IADAONITISOYACHDOVAVT-ILWS-PGALGIEFLKGFRVILEELKSEGROCOO--- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILKDPROLNSSPKRTGMESQPFLNMKRETDYFVKVVPFPSIKNESNYHPFFRTRAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFLQDFCGCEVALDLWEDFSLCREGQREWVIQK----IHESQFIIVVCSKGMKYFVDK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGELITACGTEVALDILEEQVISEYGVATWVSRQRQEMVESNSKIIILGSRG-----TQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKHKGG------GRGSGKGELFLVAVSAIAEKLRQAKOSSSAALSKFIAVYFDY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQD-------GEAR 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALDGSAALQPILHTVKAGSPSDMP--RDS-----GIYDSSV---PSSELSLPL---- 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -EGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQ--HTRQGSRRNYFRSKSG 553
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                                                                                                                                                                                                                       RM------KAAARPRL-----CVANEGVGPASRNSGLYNITEKYDNCTTYLNPVGK. 86
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2, Application US/09022696
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400 FAQFLITACGTEVALDLIEEQYISEVGVMTHVSRQKQEMVESNSKIIILCSRG----TQ 454
                                                                                                          447 KNYKHKGG------GRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDY, 496
                                                                                                                                         497 SCREEDVPGILDLSTKYRLADNIPQLÇSHLHSRDHGLQEPGQ--HTRQGSRRNYFRSKSG 553
                                                                                                                                                                                                                                      554 RSLYVAICHWHQFIDEEPDWFEKQFVPFHP----PPLR---YREPVLEKFDSGLVLNDVM 606
                                                                                                                                                                                                                                                                                                                                                            568 ROLKEAVLREGEWOTOCRDWFERENICLADGODLPSLDEEVFEDPLLPP-GGGIVKOQPL 626
                                                                                                                                                                                                                                                                                                                                                                                                        607. CKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQD-------GEAR 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL-INFORMATION:
APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Apple Operating System 7.5. SOFTWARE: MIGROSOFT WORD for PowerMacintosh, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
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COMPUTER: Apple PowerMacintosh
ODERALING SYSTEM: Apple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08978773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 26
LECOMMUNICATION INFORMATION
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 -- LILKDPKOLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 LSMLQHHRKRWRFSF----SHFVVDPGQEYEVTVHHLPKPIPDGDPNHRSKIIFVPDC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 D---LLLLQPDNLACKPFWKPRNLNI----SQH--------GSDMQV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 EDSKMKMTTSCVSSGSLWDP-NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 CFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPF-FSSCLND-----CLR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 ONVSPGDYIIELVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 HAVTVPCPVI----SNTT-----VPKPVADYIPLWVYGLITLIAI----LLVGSVIVL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 FTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQC 3990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 SFD-----HAPHNFGFRFFYLHYKLKHE---GPFKRKTCKOEQTTETTSCLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 IICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPR-KVWIVYSA-DHPLYVEVVLK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 GWRM------KAAARPRL-----CVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGK 86
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                        SYSTEM: Apple Operating Syst
Microsoft Word for Apple, Vo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: USSN 08/410,535
23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
                                                                          ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCKET NUMBER: 24,69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: (206)587-0430 TELEFAX: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                        Seattle
                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POPOLOGY
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                                        43;
                                                                                                                                                                                                                                                                                                                                                                                      ......GSDMQV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 CFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPF-FSSCLND-----CLR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 ONVSPGDYIIELVDDTNTTRKVMHYALKPV··HSP·WA-GPIRAVAITVPLVVISAFATL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 FAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQK----IHESQFIIVVCSKGMKYFVDK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SC-EGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQ--HTRQGSRRNYFRSKSG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSLYVAICHMHQFIDEEPDWFEKQFVPFHP----PPLR---YREPVLEKFDSGLVLNDVM 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      607 CKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQD--------GEAR 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALDGSAALQPILHTVKAGSPSDMP--RDS-----GIYDSSV---PSSELSLPL----- 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 HVIADAQNITISQYACHDQVAVT-ILMS-PGALGIEFLKGFRVILEELKSEGRQCQQ----141
                                                                                                                                                                                                                      --LILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRAC 199
                                                                                                                                                                                                                                                                                                                                      132 LSMLQHHRKRWRFSF----SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                       EDSKMKMTTSCVSSGSLWDP-NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 FTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNYKHKGG------GRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 AKWKAILGWAEPAVQLRCDHWRPAGDLFTAAMNMILPDFKR-----PACFGTYVVCYFSG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627 VRELP-SDGCLVVDVCV-----SEEESRMAKLDPQLWPQRELVAHTLQSMVLPAEQV 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFD-----HAPHNFGFRFFYLHYKLKHE---GPFKRKTCKQEQTTETTSCLL 274
                                                                                                                                  17 GWLLILLINVLAPGRASPRILDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPRNI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        693 ----MEGLSTDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSYTDE 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 GWRM-----KAAARPRL-----CVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGK, 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fansilow, William
TITLE OF INVENTION: 00. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
             milarity 22.5%; Pred. No. 8.2e-23; Conservative 128; Mismatches 319; Indels
                                                                                                                                                                                                                                                                                                                                                                                         200 D---LLLQPDNLACKPFWKPRNLNI----SQH-----
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09022253 Patent No. 6096305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex C
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us-09-022-253-2
                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        554
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132 LSMLQHHRKRWRFSF----SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDC 185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 --LILKDPRQLNSSFKRTGMESQPFLNMKPETDYFVKVVPEPSIKNESNYHPFFFRTRAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D---LLLQPDNLACKPFWKPRNLNI----SQH--------GSDMQV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : : : | | (: : : | | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 QNVSPGDYIIELVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 FTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRRVFLCYSSKDGQNHMNVVQC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAYFLQDFCGCEVALDLWEDFSLCREGGREWVIQK----IHESQFIIVVCSKGMKYFVDK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87. HVIADAQNITISQYACHDQVAVT-ILMS-PGALGIEFLKGFRVILKELKSEGRQCQQ--- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GWLLLLLINVLAPGRASPRILDPPAPVCAQEGLSCRVKNSTCLDDSWIHPRNLTPSSPKNI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 FAQFLITACGIEVALDLLEEQVISEVGVMTWVSRQRQENVESNSKIIILCSRG----TQ
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7.6%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 8.2e-23;
Matches 189; Conservative 128; Mismatches 319; Indels 203;
                                                                                                                                                                                                                                                                                                        Apple Operating System 7.5.5
t Word for Apple, Version 6.0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/620,694
FILING DATE: 21.MARCH:1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                         05/09/022,253
                                                                                                                                                                                                                                                           Apple Power Macintosh
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [206]587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 864 amino acids amino acids
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6 9	447 KNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDY 496 	, <del></del>	US-09-022-260-2 Query Match Best Local Similarity Matches 189; Conser
	497 SC.EGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPQQHTRQGSRRNYFRSKSG 553               : ::::        :: :             510 ICSERDVPDLFNITSRYPLMDRFEEVYFRIQDLEWFEPGRMHHVRELTGDNYLQSPSG 567	· .•	0.4
5 g	554 RSLIVAICNHHOFIDEEPDWFEKGFVPFHPPPLRYREPVLEKFDSGLVLNDVM 606	<del></del>	17 GWLLLL 87 HVIADA
2 A	607 CKPQPRSDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEAR 648	• • • • • • • • • • • • • • • • • • • •	142
6	649 PALDGSAALQPLLHTVKAGSPSDMP-RDSGIYDSSVPSSELSLPL 692    : ::		Db 132 LSMLQHHRKRWRF. Qy 200 DLLLQPDNLAC
S qq	693MEGLSTDOTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDE 746 735 MSPDHLQGDAREQLESLMLSVLQQSLSGQPLESWPR-PEVVLEGCTPSEEE 784		Db 186 EDSKMKTTSCVS: QY 231 SFD Db 245 CFDVVKOIFAPROI
RESULT US-09-	14 022-260-	<del>.</del>	275
D is is	2,8 <b>2</b> .	· · ·	DD 297 HAVTVPCPVI QY 331 FTVMCRKKQQENIX
• • •-	APPLICANT: Yao, Zhengbin APPLICANT: Sprigs, Melanie APPLICANT: Fanslow William	•	: :   Db 342 IICMTWRLSGADQI
	NVENTION: SEQUENCES:	• :	Oy 391 FAYFLODFCGCEV
	ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seatile	•	447
	E	• . •	Db 455 AKWKAILGWAEPAY
	ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk		Qy 497 SC-EGDVPGILDLA             : : :   Db 510 ICSERDVPDLENI
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	PEPLICATION WUMBER: 08/620,694 FILING DATE: CLASSIFICATION:	<u>.</u>	649 PAL
	PALCA APPLICATION DATA: APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995		Db 678 PAAHVVEPLHI Qy 693MEGLSTDQ
	CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia Anne		Db 735 MSPDHLQGDAREQ
	REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2617-B TELECOMUNICATION INFORMATION: TELEPHONE: (206)587-0430	· 	
	G. E. 2		CANA
	TOPOLOGI: Innear MOLECULE TYPE: protein	i,	HITLE OF INVENTION HUMBER OF SEQUENCES

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7.6%; Score 306; DB 3; Length 864;
Y 22.5%; Pred. No. 8.2e-23;
rvative 128; Mismatches 319; Indels 203; Gaps 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHTVKAGSPSDMP--RDS-----GIYDSSV---PSSELSLPL----- 692
                                                                                                                                                                                                                                                                                                                                                                                                ----HAPHNEGERFFYLHYKLKHE---GPFKRKTCKQEQTTETTSCLL 274
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                                                                                                                                                           OYACHDOVAVT-ILWS-PGALGIEFLKGFRVILEELKSEGROCOO--- 141
                                                                                                                                                                                     STQHGELVPVLHVEWTLQTDASILYLEGAELSVLQINTNERLCVKFQF 131
                                                                                                                                                                                                                                                                                                                      ACKPEWKPRNLNI ---- SQH-------GSDMQV 230
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                                                                                                           GRASPRILDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNI 76
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λO	447	KGGGRGS(	96
ąg G	455	455 AKWRAILGWAEPAVQLRCDHWKPAGDLFTAAMNMILPDFKRPACFGTYVVCYFSG 5	509
ογ	497	497 SC-EGDVPGILDLSTRYRLADNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSG 5	553
QC .	510	510 ICSERDVPDLENITSRYPLMDREEEVYFRIQDLEMFERGRMHHVRELTGDNYLQSPSG 567	267
Oy.	554	554 RSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVM 606	909
Q	. 268	568. RQLKEAVLREQEWQTQCPDWFERENLCLADGQDLPSLDEEVFEDFLLPP-GGGIVKQQPL 626	. 929
οy	607	607 CKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQD-;;;;GEAR 648	648
q	627	627 VRELP-SDGCLVVDVCVSERESRMAKLDPOLWPORELVAHTLQSMVLPAEQV 677	213
δλ	649	649 PALDGSAALQPLLHTVKAGSPSDMPRDS6IYDSSVPSSELSLPL 692	692
qa	678	678 PAAHVVEPLHLPDGSGAAAQLPMTEDSEACPLLGVQRNSILCLPVDSDDLPLCSTPM 734	734.
Qy	693	MEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDE 746	46
qq	735	735 MSPDHLQGDAREQLESIMISVLQQSLSGQPLESWPR-PEVVLEGCTPSEEE 784	. 78

Search completed: May 6, 2003, 13:46:17 Job time : 34 secs

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(without alignments) 2707.245 Million cell updates/sec
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4013
1 MAPWIQLCSVFFIVNACLNG......CKÅDLGCRSYIDELHAVAPL 753
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Published\_Applications\_AA: Database

Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%

/cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep pubpaa/US10\_NEW\_PUB IA/US07\_NEW\_PUB

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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TILE OF INVENTION: Human Cytokine Receptor PILE REFERENCE: 00-49 NUMBER OF SEQ ID NOS: 13 SOFWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: .753. CURRENT APPLICATION NUMBER: US/09/912,157 Application US/09912157 0020165348A1 CURRENT FILING DATE: Sequence

ALIGNMENTS

ö Length 753; Indels 0 Score 4013; DB 9; Mismatches Matches 753; Conservative 0; 100.0%; Query Match Best Local Similarity

ORGANISM: Homo saptens

US-09-912-157-2

61 ASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSPGALGIE 120 181 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240 61 ASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120 121 FLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFRRTGMESQPFLNMKFETDYFVKVVPF 180 181 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNI.NISQHGSDMQVSFDHAPHNFG 240 1 MAPWIOLCSVFFTVNACLINGSOLAVAAGGSGRARGADTCGWRMKAAARPRICVANEGVGP 60 1 MAPWIQICSVFFTVNACINGSQLAVAAGGSGRARGADTCGWRMKAAARPRICVANEGVGP 60 a õ . දි ŏ 윱 Š 8 ć

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541. QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600
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                                               481 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540
                                                                                                                                                                                                                                                                                                                                                                            601. VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660
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                              FRFFYLHYKLKHEGPFKRATCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
                                                                                       LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKRQQENIYSHLDEESSESSTYTAA 360
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Pred. No. 0;
0; Mismatches 0;
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APPLICANT: Ruesther, Rolf E.
APPLICANT: Gao Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 753
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Sequence 8, Application US/09912157
Patent No. US20020165348A1
GENERAL INFORMATION:
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Best Local Similarity 98.1%;
Matches 739; Conservative (
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US-09-912-157-8
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241 FRFFYLHTKLKHEGPFKRKTCKGEGTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
                                                                                                  LPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420
                                            WVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480
                                                                                                                                                                                                                  LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360
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APPLICANT: Presnell, Scott R.
APPLICANT: Ruestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT PILING DATE: 2001-07-23
NUMBER OF SEO ID NOS: 13
SOFTWARE: FeatSEO, for Windows Version 3.0
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Patent No. US20020165348A1
GENERAL INFORMATION:
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US-09-912-157-5
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61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120
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14; Gaps
                                                                             1 MAPWIQICSVFFTVNACINGSQLAVAAGGSGRARGADTCGWRMKAAARPRICVANEGVGP 60
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OY 61 ASRNSGINITEKIDNCTTYLNPVGKHVIADAQNITISOYACHD	QY 121 FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFRRTGMESQPF DD 107 FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFRRTGMESQPF	. 181	Db 167 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQH Qy 241 FRFFYLHYKLKHEGPFRRRTCKQEQTTETTSCLLQNVSPGDYII	227	Qy 301 LKPVHSPWAGPIRNYAITYPLVYISAFATLFTYMCRKRQCENIX [1]   [1	QY 361 LPREKLRPREVFLCXSSKDGONHANVYCFAYFLQDFCGCEVA  [11111111111111111111111111111111111	421	Db 407 WVIQKIHESQFIIVVCSKGMKYEVDKKNYKHKGGGRGSGKGELF Qy 481 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSH	467		Cy 601 VLNDVMCKGPESPECLKYEAAVLGATGPADSGHESGHGGLDQD 11111111111111111111111111111111111	OY 661 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLAHGLSTDOTETS	DD 647 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETS	Oy 721 PPALPSKLLSSGSCKADLGCRSTTDELHAVAP 752	RESULT 5	US-09-8/4-3013-18 Sequence 18 Application US/09874503 ; Patent No. US20020177188A1	GENERAL INFORMATION: FAPPLICANT: Chen, Jian APPLICANT: Filvaroff.Ellen	; APPLICANT: Fong, Sherman ; APPLICANT: Goddard, Audrey ; APPLICANT: Godowski, Paul J	Grimaldi, J.Chr Gurney, Austin	. A		<pre>F: Watanabe F: Williams F: Wood, Wil F: Yansura,</pre>	¥.
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		227 FREFILHYKLKHEGPFRENTCKOBOTTETTSCLLONVSPGDYILELVDDTHTRKYMHYA	OY 301 LKPVHSPWÄGPIRAVAITVPLVVISAFATLETVMCRKRODENIYSHLDEESSESSTYTAA 360 DD 287 LKPVHSPWÄGPIRAVAITVPLVVISAFATLETVMCRKRODENIYSHLDEESSESSTYTAA 346	361 LPRERLRPREVVELCTSSKDGQNHMNVVQCFAYFLQDFCQFVALDLWEDFSLCREGQRE	DD 34 TARKEKLARPRVELZISSEDGONHMNVVQCRAXFLQDFCGCEVALDLWEDFSLCREGGRE 406 QY 421 WVLQKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGGKGELFLVAVSAIAEKLRQAKQ 480 [111111111111111111111111111111111111	Db 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 466 OY 481 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGGHTR 540	467 SSSAALSKFIAVEDYSCEGDVPGILDLSTKYRLÆDNLPQLCSHLHSRDHGLQEPGQHTR	OY 541 QGSRRNYERSKSGRSLXVALCNMHQFIDEEPDWFERQFVPFHPPPLRKREPVLEKEDSGL 600	OY 601 VLNDVNCKPGPESDPCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660 Db 587 VLNDVNCKPGPESDPCLKYVBAAVLGATGPADSQHESQHGGLADGDGBARPALGATGPA	661 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE	Db 647 LHTVVRAGSPSDMPRDSGIYDSSVPSSELSLFLMRGLSTDQTETSSLTESVSSSGLGEEE 706 QY 721 PPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 753	Db 707 PPALPSKLLSSGSCRADLGCRSYTDELHAVAPL 739	RESULT 4	US-09-809-567-2; Sequence 2, Application US/09809567; Patent No. US2002004513A1; FRNERAL: YNFORMATION:		CURRENT APPLICATION NUMBER: US/09/809,567 CURRENT PILING DATE: 2001-03-15	; PRIOR APPLICATION WHOER: 09/724,460 ; PRIOR FILING DATE: 2000-11-20 ; PRIOR APPLICATION WHOER: 60/189,816	; PRION FILING DATE: 2000-03-16; NUMBER OF SEQ ID NOS: 17; SOFTWARE: Patentin Ver. 2.0	; SEQ ID NO 2 . LENGTH: 738 . WYDE: DDM	) ORGANISM: Homo sapiens US-09-809-567-2	Query Match Best Local Similarity 97.6%; Pred. No. 0; Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps	OY 1 MAPWIQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60	

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AND THERAPEUTIC USES THEREOF
QHGSDMQVSFDHAPHNFG 240
                                                                     VALDLWEDFSLCREGORE 420
                                                                                   PPPLRYREPVLEKFDSGL 600
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ORGANISM: Homo Sapien

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2000-12-20
UMBER: US PCT/US00/32678
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UNMBER: US PCT/US00/05841
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US 09/311,832
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US 60/131,022
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NGER: US 09/380,142
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TIMBER: US 60/242,837
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MBER: US 60/191,007
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IMBER: US 60/172,096
                                                                                                      ATION NUMBER: US 60/175,481
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                                                                                 42 RMKAAARPRICVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISOY 100
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                                                                                                        3 RASASGVPALFVSGEQGVGFASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY
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  Length 728;
Score 3703; DB 9;
Pred. No. 2.9e+307;
2; Mismatches B;
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                      Best Local Similarity 96.7
Matches 702; Conservative
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US-10-000-157-18
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                                                                     APPLICATION NUMBER: PCT/USO0/30873
PLING DAFE: 2000-11-10
APPLICATION NUMBER: PCT/USO0/32678
FILING DATE: 2000-12-01
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TITING DATE: 2000-03-21
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LENGTH: 728
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US-10-000-157-18
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Pred. No. 2.9e-307;
2; Mismatches 8;
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R APPLICATION NUMBER: US 09/644,848

R FILING DATE: 2000-08-22

R APPLICATION NUMBER: PCT/US00/23328

R FILING DATE: 2000-08-24

R FILING DATE: 2000-10-24

R FILING DATE: 2000-10-24

R APPLICATION NUMBER: US 60/242,837
                           APPLICATION NUMBER: US 60/191,007 FILLING DATE: 2000-03-21
                                                     APPLICATION NUMBER: PCT/USO0/07532
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APPLICATION-NUMBER: PCT/USO0/15264
PILING DATE: 2000-06-02
APPLICATION NUMBER: PCT/US00/05841
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FILING DATE: 2000-12-01
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APPLICATION NUMBER: US 60/253,646
FILING DATE: 2000-11-28
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Best Local Similarity 96.7%;
Matches 702; Conservative 2
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US-09-747-259-18
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NUMBER OF SEQ ID NOS:
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662
628. GPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSE 687
                                                                                                                             688 LSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL 747
                                                                                                                                                                                          663 LSLPLARGLSTDOTETSSLTESVSSSSGLGEREPPALPSKLLSSGSCKADLGCRSYTDEL 722
                                   ON: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTI P1381R1C1P1C1(US)
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602 687

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688 LSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL 747
                                                                                                                                                                                                                                                                                                      ALPRDRIARPOPKVPLCYSNKDGONHMNVQCFAYFLQDFCGCEVALDIWEDFSLCREGGR 406
                                                                                                                   DEEPDWFEKOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGAT
                                                                                                                                          GPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-12, Application US/09912157
Patent No. US20020165348A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 HAVAPL 753
                                                                                                                                                                                                                                                                                                                                                                                     723 HAVAPL 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mouse
US-09-912-157-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-912-157-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Si
Matches 645;
                                                                                                              568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ACHDOVAVTILMSPGALGIEFLKGFRVILEELKSEGROCOOLILKDPKOLNSSFRRTGME 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKK 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 92.3%; Score 3703; DB 9; Length 728; Best Local Similarity 96.7%; Pred. No. 2.9e-307; Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RASASGVPALFVSGEQGVGPASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQY
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854,208
PRIOR PILING DATE: 2001-05:10
PRIOR FILING DATE: 2001-05:10
PRIOR FILING DATE: 2001-05:10
PRIOR PLICATION NUMBER: PCT/US99/05028
PRIOR PELING DATE: 1999-03-08
PRIOR PLILING DATE: 1999-03-08
PRIOR PLILING DATE: 1999-05-14
PRIOR PLILING DATE: 1999-05-14
PRIOR PLILING DATE: 1999-05-14
PRIOR PLILING DATE: 1999-05-14
PRIOR PLILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR PLILING DATE: 2000-03-01
PRIOR PLILING DATE: 2000-03-01
PRIOR PLILING DATE: 2000-03-01
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 2000-06-02
PRIOR PLILING DATE: 2000-06-02
PRIOR PLILING DATE: 2000-06-02
PRIOR PLILING DATE: 2000-01-10
PRIOR PLILING DATE: 2000-01-10
PRIOR PLILING DATE: 2000-11-10
PRIOR PLILING DATE: 2000-11-10
PRIOR PLILING DATE: 2000-12-01
PRIOR PLILING DATE: 2000-12-01
PRIOR PLILING DATE: 2000-12-01
PRIOR PLILING DATE: 2000-12-02
PRIOR PLILING DATE: 2000-12-02
PRIOR PLILING DATE: 2000-12-02
PRIOR PLILING DATE: 2001-02-28
PRIOR PLING DATE: 2001-02-28
PRIOR PLING DATE: 2001-02-28
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US-09-908-827-18
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61 ASRNSGLYNITFKYDNCTTYLNP-VGRHVIADAQNITISQYACHDQVAVTILWSPGALGI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 ALKPVHSPWAGPIRAVAJTVPLVVISAFATLFTVWCRKKQQENIYSHLDEESSESSTYTA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPRERLRPRFRYFICYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQR 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAPWIQICSFFFTVNACINGSQLAVAAGGSGRARGADTCGWR------GVGP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMTAATRPRLCVANEGVGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDY I IELVDDTNTTRKVMHY
                                                                                                                                                                                                                                                                                                                                                                                                   Length 739;
                                                                                                                                                                                                                                                                                                                                                                                             Similarity 85.2%; Pred. No. 2.7e-280; 15; Conservative 37; Mismatches 53;
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION WOMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FRASESQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 739
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us-09-912-157-2.rapb

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420		qa.	335 SVILLIVCHTWRLAGEGS EKYS
407 EWAIQKIHESQFIIVVCSKGMKYFVDKKNFRHKGGSRGEAGGEFFLVAVAAIAEKLRQAK		ον	, i .
UY 450 USSAALAKETANYEDISCEGUPOFILDLSTKYRLADNILPOLCSHLHSRDHGLORP-GQH 538  UT		අ ඊ	391 YVDVYLKFAQFLLTACGTEVALDILL. 440 MXYFYDKKNYKHKGGGR
TRGGSRRNYPRSKSGRSLYVAICNNHOPIDEEDDWFEKGFYPFHPPPLRYREPVLEKFDS	,	7 <b>2</b> 0	451 TRAKWQALLGRGAPVRLR
		ď	492 VYF-DYSCEGDVPGILDLSTKYRLM
599 GLVLNDVMCKPGPESDFCLKYBAAVLGATGPADSQHFŠQHGGLDQDGBARPALDGSAA 656		a ò	502 CYFSEVSCDGDVPDLFGAAPRYPLM 549 RSKSGRSLYVAICNMHOFTDFEPDW
	<u> </u>	· · · ·	, ,
644 LQPLLHAVKAGSPSEMPRDSGIYDSSVPSSELSLPLMEGLSPPQLETSSLTESVSSSGL 703		ď	601 VLNDVMCKPGPESDFCLKVEAAVLG
717 GEBEPPALPSKLISSGSCRADIGCRSYTDELHAVAPL 753		đ	618 VKRAPLVRE-PGSQACLAIDPLVGE
TLPSKLFASGVSR-EHGCHSHTDE		δ	641 LDODGEARPALDGSAALQ
RESULT. 11		qa :	677 IVAAVEPGPLADGAAVRLALAGEGE
809-5 ence		QY	692 LMEGLSTDQTETSSLTESVSSSGL
Patent No. US20020045213A1 GENERAL INFORMATION:		q	728 LGSSTPMASPDLLPEDVR
APPLICANT: Jing, Shuqlan		ř	E
מינים מינים מינים מינים		2 55	US-09-778-971-9
CURRENT APPLICATION NUMBER: US/09/809,567 CURRENT FILING DATE: 2001-03-15		~ ;~	Sequence 9, Application US/0977899 Patent No. US20020102639A1
PRIOR APPLICATION NUMBER: 09/724,460 PRIOR FILING DATE: 2000-11-28			GENERAL INFORMATION: APPLICANT: Shaughnessy, John D.
PRIOR APPLICATION NUMBER: 60/189,816 PRIOR FILING DATE: 2000-03-16			TILE OF INVENTION: Evi27 Gene S
NUMBER OF SEG IN NOS: 17	-	·	. 5
. നയ		· · · ·	CURKENI FILING DAIE: 2001-02-02 PRIOR APPLICATION NUMBER: US 60/ DELOB PITING HATE: 2000-02-04
TYPE: PRT		· ••	20 ID 3
08-00-809-267-3			SEU ID NO 9 LENGTH: 866
•	:	:	ORGANISM: Unknown
vative 107; Mismato	• .		FEATURE: NAME/KET: peptide Owner Information: II-17 recent.
69 NITEKIDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMS 113		ŭ	
49 NCTVKNSTCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWT 99			h 24-17-17-18-18-18-18-18-18-18-18-18-18-18-18-18-
114 - PGALGIEFIKGFRVILEELKSEGRQCQQLILKDPKQINSSFRRTGMESQPFLNNKFETD 172			Best Local Similarity 23:18; 'F Matches 178; Conservative 107;
100 LOTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFV-VDPDQE 156		Oy	69 NITERYDNCTTYLNPVGKHVIAD
173 YEVKVVPEPSIKNESNYHPFFFRTRACDLILQPDNLACKPFWKPRNL 219		<b>a</b>	49 NCTVKNSTCLDDSWIHP
157 YEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLMDP-NITVETLEAH 215		δ.	114 -PGALGIEFLKGFRVILEELKSEGR
220NISOHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 270	·	a	100 LOTDASILYLEGAELSVLOLNTNER
216 QLRVSFTLANESTHYQILLTSFPHMENHSCFEHMH-HIPPAFRPEEFHQRSNVTLTLRNLK 274		ď	173 YFVKV - VPFPSIKNESNYHPFFFR
SCLLQNVSPGDYILELVDDTNTTRKVHHYALKPVHSPHAGPIRAVAITVPLVVISAF		a a	
275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLMVYWFITGISILLVG 334		ογ	220NISOHGSDMQVSFDHA
328 AILFTVMCKKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQN 383		<b>ਰ</b> ੁੱ	216 OLRYSFILWNESTHYOILLISFPHM

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WEDFSLCREGOREWV -- TONIBESOFILVVCSKG 439
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Pred. No. 9.1e-18;
7; Mismatches 338; Indels 146; Gaps 34;
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EEGGAAVAKLEPHLQPRGQPAPQPLHTLVLAAEEGA 676
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L-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
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                                          216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEEFHQRSNVTLTLRNLK 274
                                                                                                                                                         327
                                                                                                                                                                                                    275 GCCRHQYQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLMYYWFITGISILLVG 334
                                                                                                                                                                                                                                                                                                          328 ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRP----KVFLCYSSKDGQN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 HMNVVQCFAYFLQDFCGCEVALDLMEDFSLCREGOREMV----IQKIHESOFIIVVCSKG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 MKYFVDKKNYKHKGGG-----RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKR-----PACFGTYVV 501
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                                                                                                                                                         SCLLONVSPGDYIIELVDDT - - - NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF
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    -----NISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT
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CURRENT FILING DATE: 2001-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/244,072
PRIOR FILING DATE: 2000-10-26
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Patent No. US20020177188A1
GENERAL INFORMATION:
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Hymowitz, Sarah G.
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APPLICANT: Filvaroff, Ellen
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TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists
FILE REFERENCE: 2982-A
                                                                                                                                                                                                                                                                                                                                                         391 YYDVYLKPAQFLITACGTEVALDLLEEQAISEACYHTWYGRQKQENYESNSKIIYLCSRG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 - PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETD, 172
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                                                                                                                                                                                                                                                                                                              384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGOREWV----IQKIHESQFIIVVCSKG 439
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                                                   275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLMYYWFITGISILLVG 334
                                                                                                                                                     328 ATLFTVMCRKKQOENIYSHLDEESSESSTYTAALPRERLRPRP----KVFLCYSSKDGON 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 MRYFYDKKNYKHKGGG------RGSGKGELFLVAVSALAEKLRQAKGSSSAALSKFIA 491
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271 SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       692 LMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGC 740
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Patent No. US20020136724A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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49; Mismatches 141; Indels 113; Gaps 14;

76; Conservative

Matches

 262 -----KQEQTTE---TTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 313

184 ITACKKNEETVEVNFTTTPL----GNRYMALIQHSTI-----IGFSQVFEPHOKKQT 231

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314 AVAITVPLVVISAFATL-------FTVMCRKRQQENIYSHLDEESSESS 355

289 GWLPLLLSLLVATWVLVAGIYLMWRHBRIKKTSFSTTTLLPPIKVLVVYPSEICFHH-- 346

356 TYTAAL------PRERLR-----PRERLR-356 TYTAAL

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LICATION NUMBER: US 60/242, the DATE: 2000-10-24 carried by MUMBER: US 60/15, the DATE: 2000-01-11 carried by MUMBER: US 60/19, the DATE: 2000-06-22 carried by MUMBER: US 60/13, the DATE: 1999-12-23; the DATE: 1999-05-14	LICATION N LING DATE:: LICATION N LICATION N	APPLICATION NUMBER: US 09/644,848  RELING DATE: 2000-18-20  RAPLICATION NUMBER: US 09/644,848  RAPLICATION NUMBER: US 09/380,142  FILING DATE: 1999-08-25  RELING DATE: 1999-08-25  RELING DATE: 1999-05-14  RAPLICATION NUMBER: US 09/311,832  RELING DATE: 1999-05-14  RAPLICATION NUMBER: US PCT/US01/06520  RILING DATE: 2001-02-28  RAPLICATION NUMBER: US PCT/US00/34956  FILING DATE: 2000-12-20  RAPLICATION NUMBER: US PCT/US00/32678  RELING DATE: 2000-12-01  RAPLICATION NUMBER: US PCT/US00/32678  RELING DATE: 2000-11-10  RAPLICATION NUMBER: US PCT/US00/3328  RELING DATE: 2000-11-10  REPLICATION NUMBER: US PCT/US00/23328  RELING DATE: 2000-11-10  REPLICATION NUMBER: US PCT/US00/23328  RELING DATE: 2000-11-10  REPLICATION NUMBER: US PCT/US00/23328  RELING DATE: 2000-01-00-00-00-00-00-00-00-00-00-00-00-	ATION NUMBER: US DATE: 2000-03-2 ATION NUMBER: US DATE: 2000-03-0 ATION NUMBER: US DATE: 2000-03-0 DATE: 1999-12-3 ATION NUMBER: US DATE: 1999-12-3 ATION NUMBER: US DATE: 1999-05-11-3 ATION NUMBER: US DATE: 1999-05-10 DATE: 1999-05-05-10 DATE: 1999-05-05-05-05-05-05-05-05-05-05-05-05-05-
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447 KNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGIL 506

347 TICYFTEFLONHCRSEVILEKWOKKKIAEMGPVOWLATOKKAADKVVFLLSNDVNSVCDG 406

387 VVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDK 446

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Qy 507 DISTRICT RILDORLE-CICSH. 525

Db 461 SVCPKYHLAKDATAFCAEL 479

RESULT 15

GS-10-000-157-12

GS-10-000-157-12

GSRUED INFORMATION:

APPLICANT: FILVANCIF, Rellen

APPLICANT: FILVANCIF, Rellen

APPLICANT: GLANG, Audrey

APPLICANT: Hanahog, Colle

APPLICANT: Wond, Audrey

APPLICANT: Wond, Wonder: GO/13621

PRIOR PRIOR PLING DATE: 1999-06-14

PR
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3.4%; Score 135.5; DB 9; Length 502; 20.1%; Pred. No. 0.0046;

Query Match Best Local Similarity ; ORGANISM: Homo Sapien US-10-000-157-12

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; SEQ ID NO 12

14; Query Match
Best Local Similarity 20.1%; Pred: No. 0.0046;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 262 -----KOEQTTE---TISCLLQNVSPCDXIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 313 289 GWLPLLLISLLVATWYLVAGIYLAWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHH-+ 346 387 VVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDK 446 143. HANNEDGPSMSVNFTSPGCLDH-----IMKTK------KKCVKAGSLWDPN 183 184 ITACKKNETVEVNFTTTPL-----GNRYMALIQHSII-----IGFSQVFEPHQKKQT 231 314 AVAITVPLVVISAFATL------FTVMCRRKQQENIYSHLDEESSESS 355 356 TYTAAL------PRERLR-----PRERLR 386 218 NINISQHGSDMQVSF-----DHAPHNFGFRFFYLHYKLKHEGPFRRRTC----- 261 6, 2003, 13:51:05 507 DLSTKYRLMDNLPQLCSHL 525 461 SVCPKYHLMKDATAFCAEL 479 Search completed: May Job time : 28 secs q a ò ò ä g

score:

Title: Perfect sc Sequence:

Run on:

Scoring table:

Searched:

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ASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSPGALGIE 120
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Sequence 10,
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APPLICANT: Presnell, Scott R.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Goo, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REPERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILIG DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
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100.0%; Score 4013; 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches
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US-09-912-157-2
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LENGTH: 753
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                        GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-912-157-5
US-09-912-157-8
US-09-724-460-2
US-09-809-567-2
US-10-216-156-2
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.Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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61 ASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQYACHDQYAVTILWSPGALGIE 120
                                                                                  241. FREFYLHYKLKHEGPFKRKTCKOEGTTETTSCLLONVSPGDYITELVDDTNITRKVMHYA. 300
                                                                                                                                                            LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQ#NIYSHLDEESSESSTYTAA 360
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                        121 FLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNNKFETDYFVKVVPF 180
                                     PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWRPRNLNISQHGSDMQVSFDHAPHNFG 240
                                                                                                                                 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTR 540
                                                                                                                                                                                                                                                                                                                                                         OGSRRNYFRSKSGRSLYVAICHMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600
                                                                                                                                                                                                                                                                                                                                                                         LPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.8%; Score 4003; DB 23; Length 753; Best Local Similarity 99.7%; Pred. No. 0; Matches 751; Conservative 0; Mismatches 2; Indels 0
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| SGUERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Presentl., Scott R.
| APPLICANT: Resenter, Rolf E.
| APPLICANT: Geo. Zeren
| TITLE OF INVENTION: Human Cytckine Receptor
| FILE REFERENCE: 00-49
| CURRENT FILING DATE: 2001-07-23
| WUNBER OF SEQ ID NOS: 13
| SOFTWARE: FRSESEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-157-5
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US-09-912-157-5
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                                                    - 121 FLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESQPFLAMKFETDYFVKVVPF 180
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APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor PILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
KUMBER OF SEQ ID NOS: 13
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Sequence 8, Application US/09912157
GENERAL INFORMATION:
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US-09-912-157-8
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Matches 739; Conserv
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LENGTH: 739
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Best Local Similarity 97.6
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GENERAL INFORMATION:
APPLICANT: Jing, Shuqian
TITLE OF INVENTION: IL-17 Receptor Like Molecules and
FILE REFERENCE: 01017/36916
CURRENT APPLICATION NUMBER: 05/09/724,460
CURRENT APPLICATION NUMBER: 60/189,816
PRIOR APPLICATION NUMBER: 60/189,816
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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US-09-724-460-2
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                                 1 MAPWLQLCSVFFTYNACLNGSQLAVAAGGSGRARGADTCGWRWRAAARPRLCVANEGVGP 60
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GENERAL INFORMATION:
APPLICANT: JION:
APPLICANT: JION:
ALITLE OF INVERTION: IL-17 Receptor Like Molecules and Uses Thereof
FILE REFERENCE: 01017/36916A
1; Mismatches
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CURRENT FILING DATE: 2011-03-15
PRIOR APPLICATION NUMBER: 09/724,460
PRIOR PILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ. ID NOS: 17
SOFTWARE: PALEGILIN Ver. 2.0
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US-09-809-567-2
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FILING DATE: 2000-11-28

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PRIOR APPLICATION NUMBER: 60/189,816
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS:17
SOFWARE: Patentin Ver. 2.0
                                                                             TYPE: PRT ORGANISM: Homo saptens
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                                                                 LENGTH: 738
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US-10-216-156-2
Sequence 2, Application US/10216156
GENERAL INFORMATION:
TITLE OF INFUNITON: IL-17 Receptor Like Molecules and Uses Thereof
FILE REPERENCE: 01017/36916A
CURRENT APPLICATION NUMBER: US/10/216,156
CURRENT FILING DATE: 2002-08-08
                                                                 Indels 14;
                                           Length 738;
                                           DB 22;
                                                                 1; : Mismatches
                                            Score 3901;
Pred. No. 0;
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PRIOR FILLING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/724,460
                                          97.28;
                                                                Matches 1734; Conservative
           : Homo saplens
                                                       Best Local Similarity
                                            Query-Match 5:
                   US-09-809-567-2
TYPE:
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ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSPGALGIE 106
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                                                                                                                                                                                                                      OGSRRNYFRSKSGRSLYVALCNMHOFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 600
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                                                                                                              61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSPCALGIE 120
                                                                                                                                                                    121. FLKGFRVILEELKSEGROCOOLIILKDPROLNSSFKRTGMESQPFLNMKPETDYFVVVVPF 180
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                              14; Gaps
                                                         MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60
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                               Indels
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                                                                           1. MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRAWGVDTCGWR-
    80
   ; Score 3901; DB
; Pred. No. 0;
1; Mismatches
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 97.2%;
    Query Match
Best Local Similarity 97.6
Matches 734; Conservative
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US-09-863-818A-10
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LPRERLRPRPRVFLCYSSKDGONHMNVVOCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
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                                                                                         226 FRFFYLHYKLKHEGPFKRKTCKQEGTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 285
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99.7%; Pred. No. 0;
ive 1; Mismatches
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Sequence 3399, Application US/10104047
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
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CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3399
LENGTH: 728
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Matches 696, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys. KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CON: (120)..(120)
INFORMATION: The 'Xaa' at location 120 stands for lle, Val, Leu, or Phe.
TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS FILE REFERENCE: DX01170K
CURRENT APPLICATION NUMBER: US/09/863,818A
CURRENT FILIGO DATE: 2001-05-23
PRIOR FILITION DATE: 2000-05-24
NUMBER: OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3:1
SEQ ID NO 10
LENGTH: 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120
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Pred. No. 0;
2; Mismatches 10; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, NAME/KET: misc_feature.
LOCATION: (109)...(109).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fON: (134)..(134)
INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
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OTHER INFORMATION: unknown amino
NAME/KEY: misc_feature
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INFORMATION: unknown amino
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FHER INFORMATION: unknown amino
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HER INFORMATION: unknown amino
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OTHER INFORMATION: unknown amino
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Best Local Similarity 96.4%;
Matches 726; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo saptens
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LOCATION: (144). (144)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOHTROGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEK 595
                              356 TYTAALPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCR 415
                                                                                                                                                                                                                                                                                   VMHYALKPVHSPWAGPIRAVAITVPLVVISAEATLFTVMCRKKQGENIYSHLDEESSESS 355
                                                                                                                                                  EGOREWVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKL 475
                                                                                                                                                                                                                                                                                                                                                                           535
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                                                                                                                                                                                                                                                                                                                                                                        476 ROAKOSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: P1381R1C1P1(US)
CURRENT APPLICATION NUMBER: US/09/747,259
CURRENT FILING DATE: 2000-12-20
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APPLICATION NUMBER: US 60/172,096
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TWBER: US 60/191,007
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APPLICATION NUMBER: US 60/175,481
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Filvaroff, Ellen
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ENTION: IL-17 P
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APPLICATION NUMBER:
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US-09-747-259-18
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101 ACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGME 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 RMKAAARPRICVANE-GVGPASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQY 100
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96.7%; Pred. No. 0;
tive 2; Mismatches
              APPLICATION NUMBER: PCT/US00/15264 PFILING DATE: 2000-06-02
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PRIOR FLING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR: APPLICATION NUMBER: PCT/US00/32678
                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
                                   PRIOR FILING DATE: 2000-00-00
PRIOR APPLICATION NOMBER: 05.60/213,087
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 05.09/644,848
PRIOR FILING DATE: 2000-08-32
                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                      APPLICATION NUMBER: US 60/242,837
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1000-03-2
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Matches 702; Conservative
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SEQ:ID NO 18
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CON: 1L-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF P1381R1C1P3(US)
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                                                                                                                                                                                                                               628 GPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSE 687
                                                                                                                                                                         543 DEEDDWFEKQFVPPHPPPLATREPVLEKFDSGLVLADVMCKFQFESDFCLKVEAAVLGAT
  448 NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD
                                       423 NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD
                                                                                                                                                        568 DEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGAT
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                                                                             508 LSTRYRLMDNLPQLCSHLHSRDHGLQEPGOHTRQGSRRNYFRSKSGRSLYVAICNMHQFI
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CURRENT APPLICATION WINBER: US/5/09/874,503
CURRENT: FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/253,646
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FILING DATE: 2000-10-26
APPLICATION NUMBER: US 60/242,837
FILING DATE: 2000-10-24
APPLICATION NUMBER: US 60/175,481
PILING DATE: 2000-01-11
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FILING DATE: 2000-06-22
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FILING DATE: 1999-06-09
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Hymowitz, Sarah G.
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TITLE:OF INVENTION: IL-17 HOWOLOGOUS POLIPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE::P1381RIC1P2(US)
CURRENT APPLICATION NUMBER: US/99/816,744
CURRENT:FILING DATE: 2001-03-22
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NUMBER OF SEQ ID NOS: 39
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2; Mismatches
                                                                                                                                                                                                              Sequence:18, Application:US/09816744 GENERAL INFORMATION:
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Vandlen, Richard
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Williams, P. Mickey
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APPLICANT: Filvaroff, Ellen
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Best Local Similarity, 96.77
Matches 702, Conservative
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Goddard, Audrey
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Lllan, Kenneth
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US-09-816-744-18
                                                            748 HAVAPL 753
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APPLICANT:
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TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREO!
FILE REFERENCE: P1381R1C1P1C1(US)
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   NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKOSSSAALSKFIAVYFDYSCEGDVPGILD
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Grimaldi, Christophe
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96.7%; Pred. No. 0;
tive 2; Mismatches
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                                                                                                                                                                                                                                                                                       US 09/311,832
                                                                                                APPLICATION NUMBER: US 09/854,280:
                                                                US. 09/854, 208
                                                                                                                              US 09/816,744
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US-09-874-503-18
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; Pred. No. 0;
2; Mismatches 8; Indels 14
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/311,812
PRIOR APLICATION NUMBER: 09/380,138
PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380,142
PRIOR FILING DATE: 1999-06-25
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PRIOR FILING DATE: 1999-06-25
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PRIOR PILING DATE: 2001-05-10
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           60/172,096
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                                                   ICATION NUMBER: 60/175,481
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; ORGANISM: Homo Sapien
US-09-908-827-18
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TITLE OF INVENTION: 11-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P1C1(US)
CURRENT APPLICATION NUMBER: US/09/908,827A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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123 SOPELNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLOPDNLACKPFWKPRNLN
                                                                                                                   221.ISQ-------HGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFRRKTCKQEQTT
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PRIOR FILING DATE: 1998-12-23
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GENERAL INFO
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268 ETTSCILQHVSPGDYIIELVDDTNTTRKVHHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
243 ENTSCILQHVSPGDYIIELVDDTNTTRKVHYALKPVHSPWAGPIRAVAITVPLVVISAF 302
                                                                                                                                                                                                                                                                                                                                                                                             101 ACHDQVAVTILWSPGALGIEFLKGFRVILEELKSBGRQCQQLILKDPKQLNSSFKRTGME 160
                                                                             63 ACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDFRQLNSSFRRTGME 122
                                                                                                                                           123 SQPFLNHKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKFRNLN 182
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Godowski, Paul L.
Grimaldi, J.Christopher
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Li, Hanzhong
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723 HAVAPL, 728
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LING DATE: 1999-03-08
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PRIOR APPLICATION NUMBER: PCT/US01/06520
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JING DATE: 1999-12-30
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FILING DATE: 2000-03-21
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LING DATE: 2000-06-02
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                                  LICATION NUMBER: 60/131,022:
                                                                                                                                                                                                                                                                                                                                                                                                             PLICATION NUMBER: 09/644,848
LING DATE: 2000-08-22
PLICATION NUMBER: 09/747,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LICATION NUMBER: 09/854,208
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                                                                                                                                                                                                                                                                                      PLICATION, NUMBER: 60/244, 072
                                                                                                                                                                                                                                                                                                                  PLICATION NUMBER: 09/311,832
LING DATE: 1999-05-14
   60/130,232
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FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                 PLICATION NUMBER: 09/380,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LICATION NUMBER: 09/816,744
                                                             60/134,287
                                                                                              NUMBER: 60/138,387
                                                                                                                                                            APPLICATION NUMBER: 60/175,481
                                                                                                                                                                                           NUMBER: 60/191,007
                                                                                                                                                                                                                       FLICATION NUMBER: 60/213,807
LING DATE: 2000-06-22
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Best Local Similarity 96.7%;
Matches 702; Conservative
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PRIOR APPLICATION NUMBER: PCT
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ORGANISM: Homo Saplen
US-09-908-827A;18
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LENGTH: 728
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PPLICANT: Yansura, Daniel
ILL17 HOWOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
ILLE REFERENCE: P13491RICTP4 (US)
TREENT APPLICATION NUMBER: US/10/000,157
BREWT APPLICATION NUMBER: 05/0065579
SION PPLICATION NUMBER: 60/0065579
SION PILING DATE: 1998-05-15
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FILING DATE: 2000-02-18
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05-14
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APPLICATION NUMBER: 60/113621
FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/130232
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FILING DATE: 2001-05-10.
APPLICATION NUMBER: 09/874503
FILING DATE: 2001-06-05
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APPLICATION NUMBER: 60/131022
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ING DATE: 2000-10-26
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LICATION NUMBER: 09/380138
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NG DATE: 1999-08-25
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LING DATE: 2000-12-20
PPLICATION NUMBER: 09/816744
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APPLICATION NUMBER: 09/931836
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42 RMKAAARPRICVANE-GVGPASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQY 100
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Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8;
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR PELICATION NUMBER: PCT/US00/310873
PRIOR APPLICATION NUMBER: PCT/US00/31678
PRIOR PELICATION NUMBER: PCT/US00/31678
PRIOR FILING DATE: 2000-12-01
PRIOR PELICATION NUMBER: PCT/US00/34956
PRIOR PELICATION NUMBER: PCT/US01/0520
PRIOR PELICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR PELICATION NUMBER: PCT/US01/19692
PRIOR PELICATION NUMBER: PCT/US01/19692
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR APPLICATION NUMBER: PCT/US01/1369
PRIOR PELING DATE: 2001-06-20
PRIOR PELING DATE: 2001-06-20
PRIOR PELING DATE: 2001-06-20
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SEQ ID NO 18
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US-10-000-157-18
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              BFLKGFRVILEELKSEGROCQQLILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVP 179
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APPLICANT: Fresnell, Scott R.
APPLICANT: Fuestner, Rolf E.
APPLICANT: Gao, Zeren
TILLE OF: INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.4%; Score 3387; DE Best Local Similarity 85.2%; Pred. No. 0; Matches 645; Conservative 37; Mismatches
                                                                                                                                                                         Sequence 12, Application US/09912157 GENERAL INFORMATION:
                                                                                 HAVAPL 728
                                                             748 HAVAPL 753
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; ORGANISM: Mouse
US-09-912-157-12
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LENGTH: 739
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